

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 18 Seconds

(without alignments)
1554.173 Million cell updates/sec

Title: US-09-424-705b-2

Perfect score: 1536
Sequence: 1 MKYLLPTAAAGLLLAQPA.....GSEQKLISEDLNHHHHH 291Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857.5	55.8	268	2 A56446	Ig heavy chain V r
2	671	43.7	249	2 S41374	single chain Fv an
3	612	39.8	233	2 JCS322	p53 specific singl
4	545	35.5	144	2 B30502	Ig heavy chain V r
5	540.5	35.2	139	2 PS0024	Ig heavy chain pre
6	531	34.6	235	2 S25058	Ig kappa chain - m
7	527	34.3	287	4 PC4402	pelb leader/Ig hea
8	521.5	34.0	246	2 S38950	Ig gamma chain - m
9	521.5	34.0	246	2 S40295	Ig gamma-2a chain
10	519	33.8	107	2 A30562	Ig kappa chain V r
11	519	33.8	474	1 G2MS11	Ig gamma-2b chain
12	514	33.5	107	2 B30502	Ig heavy chain V r
13	513.5	33.5	130	1 JL0079	Ig kappa chain pre
14	513.5	33.4	120	2 S41394	Ig heavy chain V r
15	512.5	33.4	140	2 PH1482	Ig heavy chain V r
16	511.5	33.3	139	2 A27609	Ig heavy chain pre
17	508.5	33.1	140	1 HVMG7	Ig heavy chain pre
18	508.5	33.1	103	2 S29591	Ig kappa chain V r
19	506.5	33.0	120	2 B22769	Ig heavy chain V r
20	504	32.8	104	2 B49049	Ig kappa chain V r
21	503.5	32.8	122	2 S24287	Ig heavy chain V r
22	503.5	32.8	131	2 S66537	Ig heavy chain V r
23	503.5	32.8	139	1 MMS18	Ig heavy chain pre
24	501.5	32.6	469	2 S37483	Ig gamma-2a chain
25	501	32.6	106	2 PS0071	Ig kappa chain V r
26	501	32.6	120	2 S25175	Ig heavy chain V r
27	499.5	32.5	140	2 PH1489	Ig heavy chain V r
28	497.5	32.4	108	2 G30560	Ig kappa chain V r
29	497	32.4	118	2 S38565	Ig heavy chain V r

30	496	32.3	116	2 S55542	Ig heavy chain V r
31	496	32.3	121	2 A26405	Ig heavy chain V r
32	494.5	32.2	116	2 S53751	antibody Fab Jcl 1
33	494	32.2	107	2 S11118	Ig kappa chain V r
34	494	32.2	122	2 S20643	Ig heavy chain V r
35	493.5	32.1	140	2 PH1484	Ig heavy chain V r
36	493	32.1	107	2 PT0406	Ig kappa chain V r
37	492.5	32.1	151	2 PL0011	Ig kappa chain pre
38	492	32.0	123	2 E48677	Ig heavy chain V-D
39	491	32.0	107	2 PC4405	Ig heavy chain V r
40	491	32.0	107	2 S11119	Ig kappa chain V r
41	491	32.0	138	2 E32513	Ig heavy chain pre
42	490.5	31.9	123	2 S60067	Ig heavy chain V r
43	490.5	31.9	140	2 PH1488	Ig heavy chain V r
44	490	31.9	123	2 S20646	Ig heavy chain V r
45	489.5	31.9	140	2 PH1498	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #ext_change 16-Aug-1996
C/Accession: A56446R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident
A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 55.8%; Score 857.5; DB 2; Length 268;
Best local similarity 65.3%; Pred. No. 1.4e-51;
Matches 175; Conservative 25; Mismatches 61; Indels 7; Gaps 3;

QY	21	MAQVQLQSGAEELARPQASVKSCASGTFTRYYHWKORPGGLEWIGYINPGRGT 80	
DB	1	MAQVQLQSGAEELVKKPGASVKLSCTTSSEINIKDTYHWKORPGGLEWIGRIAPANGIT 60	
QY	81	NYNQKPKDKATLTITDKSSSTAYWQLSLTSEDSAVYVCARYPDHYSLDYWGCTTLTVS 140	
DB	61	KYDPKQKATTAADTSNNAVYLQLSLTSEDAVYVCASYLTRYE-NYWGQGTIVTVS 119	
QY	141	SAKTPKLEGEFSEARVIVLTQSPAIMASPGKAVTMTCSASSSVSNWYQKSGTS 200	
DB	120	SGGGGS--GGGDSGGGSDIELTQSPAIMASLGEAVTMTCSRASSSVNFTYVQKSDAS 177	
QY	201	PKRWYDTSKLSAGVPAHFRSGSGTSYSLTISGMAEDPAATYVCOQWSSNPFTFGSGTK 260	
DB	178	PKRWYVYTHLPQGVPAHFRSGSGSGNSYSLTISMGEDPAATYVCOQFSSPTFGSGTK 227	
QY	261	LEINRADT---APTSGEQKLISEDLN 284	
DB	238	LEIKRSAHHHHHGAAGAEQKLISEDLN 265	
RESULT 2			
S41374 single chain Fv antibody - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 06-Jan-1995			
C/Accession: S41374			
R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.			
Submitted to the EMBL Data Library, January 1994			
A/Description: Construction and functional characterization of a single chain Fv antibod			
A/Reference number: S41374			

A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 43.7%; Score 671; DB 2; Length 249;

Best Local Similarity 56.0%; Pred. No. 6.9e-39; Mismatches 29; Gaps 2;
Matches 140; Conservative 29; Indels 8; Gaps 2;

Qy 23 QVQLQSGAEALRPGASVKMSCKASGYTFTRYTHMVKQRPQGQLEWIGYINPSRGYTN 82
Db 1 QVQLQSGAEALRPGASVKLSCTASGFNPKDDYIHVWKQRPKEGLEWIAIPASGNVKY 60
Qy 83 NQKFKDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSA 142
Db 61 VRFQDKATITADTSNTAYLLSLTSDTAVYCYARERDTLYSLGYWGQGTTLTVSSR 120
Qy 143 KTTPKLEGEFSEARVDIVLTQSPAIMSASPGKVTMTCSASSV-----SYMMWYQOK 196
Db 121 GGS--GGGGGGGSDIELTQSPVSVVPIGESVISCRSKSLSDYDGDYILFWFLOR 178
Qy 197 SGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYYCQOQSSNPFTFG 256
Db 179 PQSPQLLIYRMSNLASGVDPDRFSGSGSGTSFTLRISRVEAEDGVYVCMQHREYPLTFG 238
Qy 257 SGTKLEINRA 266
Db 239 AGTKLEKRA 248

RESULT 3

JC5322

p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 39.8%; Score 612; DB 2; Length 233;
Best Local Similarity 53.6%; Pred. No. 6.8e-35;
Matches 133; Conservative 26; Mismatches 63; Indels 26; Gaps 5;

Qy 27 QQSGLAEALRPGASVKMSCKASGYTFTRYTHMVKQRPQGQLEWIGYINPSRGYTNQKF 86
Db 1 QESGAEALRPGASVKLSCTTSNINYYVHWKRPQGLEWIGRIDPENGADMTSS 60
Qy 87 KDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSAKTP 146
Db 61 GVKATMTADTSNTAYLQLSLTSDTAVYCYC-----NAGMDYWGQGTTLTVSSG--- 110
Qy 147 KLEGEFSEARV-----DIVLTQSPAIMSASPGKVTMTCSASSV-----SYMMWYQO 195
Db 111 ----GGGGGGRASGGGSDIELTQSPASLVSLGQRATISCRASKSVSTSGSYMHWNOQ 166
Qy 196 KSGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYYCQOQSSNPFTF 255
Db 167 KGPQPRLLIYLVNLESGVPAHFRGSGSGTDFTLNIHPVEEDAATYYCQHIRLTREE 226
Qy 256 GSGTKLEI 263
Db 227 G-GTKLEI 233

RESULT 4

B30502

Ig heavy chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: B30502
R:Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: B30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-144 <EIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 545; DB 2; Length 144;
Best Local Similarity 65.5%; Pred. No. 1.5e-30;
Matches 108; Conservative 11; Mismatches 22; Indels 24; Gaps

Qy 23 QVQLQSGAEALRPGASVKMSCKASGYTFTRYTHMVKQRPQGQLEWIGYINPSRGYTN 82
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTITGYVHWKQRPQGQGLAWIGYINPYNDGTYK 60
Qy 83 NQKPKDKATLTDDKSSSTAYMQLSLTSDSAVYCYARYDDHYSLDYWGQGTTLTVSSA 142
Db 61 NEKFKGKATLTDDKSSSTAYTELSSLASDAAYCYAR-----GGFDYWGQGTTLT--- 111
Qy 143 KTTPKLEGEFSEARVDIVLTQSPAIMSASPGKVTMTCSASSV 187
Db 112 -----VDILLTQSPALLSVSPGERVSPFCRASQSI 141

RESULT 5

PS0024

Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A:Reference number: PS0023; MUID:89232725; PMID:3149944
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against P₁omonas
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology <IMM>
F:20/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted

Query Match 35.2%; Score 540.5; DB 2; Length 139;
Best Local Similarity 84.3%; Pred. No. 2.9e-30;
Matches 102; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 22 AQVQLQSGAEALRPGASVKMSCKASGYTFTRYTHMVKQRPQGQLEWIGYINPSRGYTN 81
Db 19 SQVQLQSGAEALRPGASVKMSCKASGYTFTRYTHMVKQRPQGQLEWIGYINPTGYTE 78
Qy 82 YNQKPKDKATLTDDKSSSTAYMQLSLTSDSAVYCYAR-YYDDHYSLDYWGQGTTLTVS 140
Db 79 YNQKPKDKATLTADKSSSTAYMQLSLTSDSAVYCYAR-YYDDHYSLDYWGQGTTLTVS 138
Qy 141 S 141
Db 139 S 139

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 14 Seconds

(without alignments)
862.115 Million cell updates/sec

Title: US-09-424-705b-2

Perfect score: 1536
Sequence: 1 MRYLLPTAAAGLLLAQPA.....GSEQKLISEEDINSHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

T number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508.5	33.1	140	1 HV02_MOUSE	P01746 mus musculu
2	508	33.1	120	1 HV03_MOUSE	P01747 mus musculu
3	503.5	32.8	139	1 HV07_MOUSE	P01751 mus musculu
4	500	32.6	107	1 KV6F_MOUSE	P04940 mus musculu
5	497	32.4	107	1 KV6J_MOUSE	P04944 mus musculu
6	495	32.2	107	1 KV6I_MOUSE	P04943 mus musculu
7	494	32.2	107	1 KV6H_MOUSE	P04942 mus musculu
8	491	32.0	107	1 KV6G_MOUSE	P04941 mus musculu
9	482.5	31.4	137	1 HV11_MOUSE	P01755 mus musculu
10	463	30.1	138	1 HV48_MOUSE	P03980 mus musculu
11	462.5	30.1	120	1 HV50_MOUSE	P06329 mus musculu
12	462	30.1	117	1 HV12_MOUSE	P01756 mus musculu
13	457	29.8	117	1 HV13_MOUSE	P01757 mus musculu
14	446	29.0	107	1 KV6B_MOUSE	P01676 mus musculu
15	446	29.0	121	1 HV01_MOUSE	P01745 mus musculu
16	443	28.8	107	1 KV6A_MOUSE	P01675 mus musculu
17	443	28.8	117	1 KV6D_MOUSE	P01748 mus musculu
18	442	28.8	107	1 KV6D_MOUSE	P01678 mus musculu
19	441	28.7	107	1 KV6C_MOUSE	P01677 mus musculu
20	440	28.6	136	1 HV15_MOUSE	P01759 mus musculu
21	436.5	28.4	118	1 HV51_MOUSE	P06330 mus musculu
22	436	28.4	117	1 HV05_MOUSE	P01749 mus musculu
23	434	28.3	117	1 HV06_MOUSE	P01750 mus musculu
24	427	27.8	108	1 KV6K_MOUSE	P04945 mus musculu
25	426	27.7	117	1 HV09_MOUSE	P01753 mus musculu
26	424	27.6	107	1 KV6E_MOUSE	P01679 mus musculu
27	422	27.5	117	1 HV49_MOUSE	P06338 mus musculu
28	420	27.3	117	1 HV10_MOUSE	P01754 mus musculu
29	412.5	26.9	147	1 HV1C_HUMAN	P01744 homo sapien
30	411.5	26.8	117	1 HV52_MOUSE	P06337 mus musculu
31	410.5	26.7	117	1 HV14_MOUSE	P01758 mus musculu
32	407	26.5	129	1 KV4A_MOUSE	P01680 mus musculu
33	389	25.3	117	1 HV1B_HUMAN	P01743 homo sapien

34	380	24.7	117	1 HV1G_HUMAN	P23083 homo sapien
35	375.5	24.4	114	1 HV00_MOUSE	P01741 mus musculu
36	349.5	22.8	111	1 KV3M_MOUSE	P01674 mus musculu
37	346.5	22.6	108	1 KV1V_HUMAN	P04430 homo sapien
38	345.5	22.5	111	1 KV3O_MOUSE	P01667 mus musculu
39	343.5	22.4	108	1 KV1O_HUMAN	P01607 homo sapien
40	342.5	22.3	111	1 KV3L_MOUSE	P01664 mus musculu
41	339.5	22.1	111	1 KV3Q_MOUSE	P01669 mus musculu
42	338.5	22.0	108	1 KV1B_HUMAN	P01594 homo sapien
43	338.5	22.0	111	1 KV3N_MOUSE	P01666 mus musculu
44	337.5	22.0	108	1 KV1P_HUMAN	P01608 homo sapien
45	335.5	21.8	119	1 HV37_MOUSE	P01807 mus musculu

ALIGNMENTS

RESULT 1	ID	HV02_MOUSE	STANDARD	PRT	140 AA.
AC	P01746;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	19 heavy chain V region 93G precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=A/J;				
RX	MEDLINE=82152818; PubMed=6801765;				
RA	Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,				
RT	Capra J.D.;				
RT	"Somatic mutation in genes for the variable portion of the				
RL	immunoglobulin heavy chain.";				
CC	Science 216:309-311(1982).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; J00493; AAA8128.1; -				
DR	PIR; A02028; HVMSG7.				
DR	HSSP; P01810; 2FBJ.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_V.				
DR	SMART; SM00406; IgV_1.				
KW	Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.				
FT	SIGNAL 1 19				
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.				
FT	NON TER 140 140				
SQ	SEQUENCE 140 AA; 15514 MW; 254ACBBE31DA5CE8 CR664;				
Query Match	33.1%; Score 508.5; DB 1; Length 140;				
Best Local Similarity	74.4%; Pred. No. 6,9e-33;				
Matches	99; Conservative				
	9; Mismatches 22; Indels 3; Gaps 2;				
QY	12 LLLLAQPM-ADVOIQSGAEIARPGASVYKSCASGTYFTTYTHMWKQKRGGLEWT 70				
DB	8 LFLSLVTAGHSEVQLOQSGAEIARPGASVYKSCASGTYFTSYGINWKQKRGGLEWT 67				
QY	71 GYNPGRGTYNYQKFKDKATLTFTDKSSSTAYVQWLSLTSDESAVYYCAR--YYDDHYSL 128				
DB	68 GYNPGRGTYNYQKFKDKATLTFTDKSSSTAYVQWLSLTSDESAVYYCARSHYGGSYDP 127				
QY	129 DWGGGCTTLTVSS 141				

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Db 128 DYWGQGTTLTVSS 140
|||||
RESULT 2
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMG7.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW NON TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 33.1%; Score 508; DB 1; Length 120;
Best Local Similarity 80.8%; Pred. No. 6.3e-33;
Matches 97; Conservative 5; Mismatches 16; Indels 2; Gaps 1;

Qy 24 VOLQSGAELAPGASVKMSCKASGYTFRTYTHMHWKQPGGLEWIGYINPSRGVTYN 83
Db 1 VOLQSGAELVAGSSVKMSCKASGYTFRTSYGINVHWKQPGGLEWIGYINPENGVTKN 60
Qy 84 QKFKDKATLTDDKSSSTAYMQLSLTSDSVAVYCAR--YYDDHYSLDYWGQGTTLTVSS 141
Db 61 EKFKGKTLTVDKSSSTAYMQLSLTSDSVAVYFCARSVYGGSYFYDYWGQGTTLTVSS 120

RESULT 3
HV07 MOUSE
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.N., Paskind M., Reth M., Inanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA

MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSP; P01810; 2FBJ
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 32.8%; Score 503.5; DB 1; Length 139;
Best Local Similarity 74.8%; Pred. No. 1.7e-32;
Matches 101; Conservative 9; Mismatches 18; Indels 7; Gaps 3;

Qy 12 LLLAAQAP--AMAOVLQSGAELAPGASVKMSCKASGYTFRTYTHMHWKQPGGLEW 69
Db 7 MLFLAATATGVHSQVLQPGQAEIVKPGASVKLSCKASGYTFRTYTHMHWKQPGGLEW 66
Qy 70 IGYINPSRGYTNQKPKDKATLTDDKSSSTAYMQLSLTSDSVAVYCARYYDDHYS-- 127
Db 67 IGRIDPNSGGTKYNEKPKSKATLTVDKPSSTAYMQLSLTSDSVAVYCAR--DYVGSS 124
Qy 128 -LDYWGQGTTLTVSS 141
Db 125 YFDYWGQGTTLTVSS 139

RESULT 4
KV6F MOUSE
ID KV6F MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGH response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 33 Seconds
(without alignments)
1816.961 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MXYLLPTAAAGLLLAQPA.....GSBQKLISEDLNHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

T number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630.5	44.9	298	11	Q9GYF0 mus musculus
2	602.5	39.2	241	11	Q921A6 mus musculus
3	551	35.9	218	11	Q925S1 mus musculus
4	531	34.6	119	5	Q9GYZ2 mus musculus
5	523	34.0	278	11	Q921K1 mus musculus
6	510	33.2	473	11	Q921K1 mus musculus
7	508	33.1	134	11	Q921K1 mus musculus
8	505	32.9	235	11	Q921K1 mus musculus
9	503	32.7	473	11	Q921K1 mus musculus
10	501.5	32.5	143	11	Q921K1 mus musculus
11	499.5	32.5	145	11	Q921K1 mus musculus
12	499.5	32.5	145	11	Q921K1 mus musculus
13	498	32.4	142	11	Q921K1 mus musculus
14	498	32.4	142	11	Q921K1 mus musculus
15	498	32.4	143	11	Q921K1 mus musculus
16	497.5	32.4	143	11	Q921K1 mus musculus

17	496.5	32.3	143	11	Q91V67 mus musculus
18	496	32.3	146	11	Q924R8 mus musculus
19	495.5	32.3	145	11	Q924R1 mus musculus
20	494	32.2	146	11	Q924Q3 mus musculus
21	492.5	32.1	143	11	Q924Q5 mus musculus
22	492.5	32.1	145	11	Q924Q6 mus musculus
23	490.5	31.9	145	11	Q924Q9 mus musculus
24	488.5	31.8	137	11	Q924R6 mus musculus
25	487.5	31.7	141	11	Q924Q4 mus musculus
26	486.5	31.7	145	11	Q924P7 mus musculus
27	484.5	31.5	145	11	Q924R3 mus musculus
28	484	31.5	140	11	Q924R2 mus musculus
29	483	31.4	144	11	Q924P5 mus musculus
30	480.5	31.3	143	11	Q924Q0 mus musculus
31	480.5	31.3	146	11	Q924L1 mus musculus
32	477	31.1	117	11	Q924X0 mus musculus
33	477	31.1	117	11	Q924X0 mus musculus
34	474.5	30.9	146	11	Q924Q8 mus musculus
35	474.5	30.9	148	11	Q91WT1 mus musculus
36	473	30.8	142	11	Q924Q2 mus musculus
37	471	30.7	168	11	Q924D9 mus musculus
38	468.5	30.5	143	11	Q924R7 mus musculus
39	467.5	30.4	109	11	Q924L7 mus musculus
40	463.5	30.2	143	11	Q91VA2 mus musculus
41	462.5	30.1	118	11	Q921C4 mus musculus
42	460.5	30.0	143	11	Q924P6 mus musculus
43	460	29.9	149	11	Q924X4 mus musculus
44	458	29.8	613	11	Q924X7 mus musculus
45	456.5	29.7	139	11	Q924R5 mus musculus

ALIGNMENTS

RESULT 1					
Q9GYF0	PRELIMINARY;	PRT;	298 AA.		
AC Q9GYF0;					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE CN 8 scfv.					
GN CN 8.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=BALB/C; TISSUE=SPLEEN;					
RX MEDLINE=20183931; PubMed=10706631;					
RA Shiohara N., Demura T., Fukuda H.;					
RT "Isolation of a vascular cell wall-specific monoclonal antibody					
RT recognizing a cell polarity by using a phage display subtraction					
RT method."					
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).					
RL EMBL; AB036341; BAA8633.1; -					
DR HSSP; P01607; IRET.					
DR InterPro; IPR003006; IG_MHC.					
DR InterPro; IPR003596; IG_V.					
DR Pfam; PF00047; IG_2.					
DR SMART; SM00406; IGV; 2.					
SO SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;					
Query Match	44.9%;	Score 690;	DB 11;	Length 298;	
Best Local Similarity	54.7%;	Pred. No. 4.8e-46;			
Matches 139;	Conservative 35;	Mismatches 72;	Indels 8;	Gaps 5;	
QY 16 AADPAAGVLOOOSGAEIAPGASVMSCKASGYTETRYTMHWVKRPPGQEWIGYINP 75					
DB 33 AADPAAGVLOOOSGAEIAPGASVMSCKASGYTETRYTMHWVKRPPGQEWIGYINP 92					
QY 76 SRGYTNVOKFKDKATLTITDKSSSTAYMQLSSITSEDSAVVYCAR--YYDDHYSLDYWCQ 133					

```
Db 93 DSSTNTYPSLKDKFIISRDNAKNTLYLQMSKVRSEDYALYCARASYI-GHSA--YWGQ 149
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 134 GTTLTVSSAKTTPKLEGEFSEARVDIVLTQSPAIMASPGKVTWTCSSASSV-SYMNW 192
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 150 GTTVTVSSGGGGS--GGGGGGGGSDIELTQSPASLSASVGETVITTCRASNIHNYLAW 207
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 193 YQKSGTSPKRWIYDTSKLGASGVPAPFRGSGTSLTISGMEADATYYCQWSSNP 252
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 YQKQKSGPQLLYNAKTLADGVPFRSGSGSTQYSLKINSLOPEDFGSYCQHFWTTP 267
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 253 FTFGSGTKLEINRA 266
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 268 YTFGGGTKLEIKRA 281
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
Q921A6
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 39.2%; Score 602.5; DB 11; Length 241;
Best Local Similarity 50.0%; Pred. No. 2.4e-39;
Matches 127; Conservative 36; Mismatches 68; Indels 23; Gaps 7;

Qy 23 QVLOQSGGELARPGASVKMSCKASGYTFTYTMHWKORPGGLEWIGYINPSRGYTN 82
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 QVKLOQSGGPELKPGTETVIRISKASGYTTTQAGQWQKMGKGLKRWIGINTHSGVP 60
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 NQKFKDKATLTITDKSSSTAYMQLSSTSDSAVYCA-----RYDDHYSLDYWGQGTTL 137
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ADDFKGRPAFSLTASTAYLQINLNKEDTATYFCARKDLRYF-----DYWGQGTIV 114
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 138 TVSSAKTTPKLEGEFSEARVDIVLTQSPAIMASPGKVTWTCSSASSV-SYMNWQOK 196
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 TVSSGGGGS--GGGGGGGGSDIELTQSPSSLSASLGKVTITCKASQDKYIAWYQHK 172
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 197 SGTSPPKRWIYDTSKLGASGVPAPFRGSGTSLTISGMEADATYYCQWSSNP 252
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 PGKGRPSAHTLIY-----IQPIPSRFSGGSGRDYSFISINLEPDIAITYCLHY-DNL 227
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 253 FTFGSGTKLEINRA 266
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 HTFGGTKLEIKRA 241
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
```

```
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240158; AAK43733.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
FT NON_TER 218
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 35.9%; Score 551; DB 11; Length 218;
Best Local Similarity 51.4%; Pred. No. 2.2e-35;
Matches 114; Conservative 35; Mismatches 63; Indels 10; Gaps 4;

Qy 21 MAQVLOQSGGELARPGASVKMSCKASGYTFTYTMHWKORPGGLEWIGYINPSRGYT 80
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAQVLOQSGGPELKPGTETVIRISKASGYTTTQAGQWQKMGKGLKRWIGINTHSGVP 60
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 81 NYNQKFKDKATLTITDKSSSTAYMQLSSTSDSAVYCA-YDDHYSLDYWGQGTTLTV 139
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 KYAEFKGRPAFSLTASTAYLQINLNKEDTATYFCMRWDYDGGFA--YWGQGTIVTV 118
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 140 SSAKTPKLEGEFSEARVDIVLTQSPAIMASPGKVTWTCSSASSV-----SYMNWYQ 194
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SSGGGGS--GGGGGGGGSDIVLTQSPASLAVSLGQRTATISCRASESDYNTIGSPMWFQ 176
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 QKSGTSPKRWIYDTSKLGASGVPAPFRGSGTSLTISGME 236
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 QKGPQPKLLIYAASKQSGVPAAGLLASGSGTDFSLNIYPNE 218
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
Q9GYZ2
ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
```

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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 39 Seconds

(without alignments)
994.255 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MYRLPTAAAGLLLAQPA.....GSEQKISEEDLNHHHHH 291

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

T number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneeqp-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneeqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1354	88.2	539	21	AA550823
2	1346.5	87.7	554	21	AA550822
3	1300.5	84.7	288	19	AAW82482
4	1208.5	78.7	288	19	AAW82316
5	1208.5	78.7	288	19	AAW82317
6	1132	73.7	409	23	AB807680
7	1132	73.7	531	21	AAV43749
8	1124	73.2	495	23	AAE22193
9	1010.5	65.8	281	20	AAW82744
10	999.5	65.1	330	22	AAW70842

11	974	63.4	246	15	AAW60522
12	964.5	62.8	309	22	AAW70841
13	963.5	62.7	239	21	AAW12563
14	963.5	62.7	239	22	AAW36826
15	957.5	62.3	599	19	AAW37132
16	957.5	62.3	599	21	AAW87477
17	952.5	62.0	599	20	AAW95462
18	947	61.7	288	20	AAW82743
19	942.5	61.2	258	22	AAW82898
20	940	61.2	291	22	AAW82043
21	933.5	60.8	256	22	AAW82897
22	928.5	60.4	270	16	AAW75119
23	919	59.8	244	16	AAW79667
24	918	59.8	305	21	AAV59265
25	918	59.8	305	21	AAV51142
26	916	59.6	422	16	AAW79872
27	914.5	59.5	423	22	AAW30695
28	912	59.4	267	20	AAW85688
29	911	59.3	244	16	AAW79873
30	908	59.1	246	16	AAW79869
31	905	58.9	244	16	AAW79868
32	904	58.9	241	20	AAW76197
33	904	58.9	241	22	AAW50019
34	901.5	58.7	483	19	AAW82315
35	901	58.7	242	16	AAW79870
36	898	58.5	553	18	AAW11508
37	898	58.5	553	22	AAW73223
38	898	58.5	553	22	AAW85455
39	898	58.5	553	22	AAW61960
40	896.5	58.4	322	22	AAW20440
41	895.5	58.3	281	19	AAW82314
42	894	58.2	276	20	AAW90227
43	889.5	57.9	271	17	AAW02293
44	888.5	57.8	242	19	AAW53881
45	886	57.7	242	16	AAW79871

ALIGNMENTS

RESULT 1	AA550823
ID	AA550823 standard; Protein; 539 AA.
AC	AA550823;
DT	18-FEB-2000 (first entry)
DE	Fv-antibody construct containing antibody 9E10 epitope protein.
DE	Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
KW	diagnosis; therapy; disease.
OS	Synthetic.
PN	DE19819846-A1.
XX	11-NOV-1999.
PD	05-MAY-1998; 98DE-1019846.
PF	05-MAY-1998; 98DE-1019846.
PR	05-MAY-1998; 98DE-1019846.
XX	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA	Little M, Kipriyanov S;
PI	WPI; 2000-024472/03.
DR	N-PSDB; AA243432.
XX	Multivalent Fv-antibody constructs with at least four variable domains
PT	connected by 1, 2 and 3 peptide linkers
XX	

PS Example 1; Fig 6; 14pp; German.

XX This invention describes a novel multivalent Fv-antibody construct with
 CC at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence represents a bivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-SL

XX Query Match 88.2%; Score 1354; DB 21; Length 539;
 PS Best Local Similarity 52.9%; Pred. No. 6.2e-80;
 XX Matches 285; Conservative 2; Mismatches 4; Indels 248; Gaps 3;

Qy 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMCKASGYTFTRYTHHWK 60
 Db 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMCKASGYTFTRYTHHWK 60

Qy 61 QPQGGLEWIGVINSRGYTNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 Db 61 QPQGGLEWIGVINSRGYTNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120

Qy 121 YYDDHSLDYWGQGTTLTVSSAKTPKL----- 148
 Db 121 YYDDHSLDYWGQGTTLTVSSAKTPKLGGDILLTQTPASLAVSLGORATISCKASQSV 180

Qy 149 ----- 148
 Db 149 ----- 148

Qy 181 YDGD SYLWYQIIPGPPKLLIYDASNLVSGIPPRFSGSGGTDFTLNHPVEKVDAA 240
 Db 181 YDGD SYLWYQIIPGPPKLLIYDASNLVSGIPPRFSGSGGTDFTLNHPVEKVDAA 240

Qy 149 ----- 148
 Db 149 ----- 148

Qy 241 HQQSTEDPWTGGGKLEIKRADAAGGPGSQVLOQSGAELVPGSSVKISCKASGY 300
 Db 241 HQQSTEDPWTGGGKLEIKRADAAGGPGSQVLOQSGAELVPGSSVKISCKASGY 300

Qy 149 ----- 153
 Db 149 ----- 153

Qy 301 AFSSYMNWVKORPGGLEWIGQIWPFGDGTNYNGKFKGKATLTADSSSTAYMQLSSLA 360
 Db 301 AFSSYMNWVKORPGGLEWIGQIWPFGDGTNYNGKFKGKATLTADSSSTAYMQLSSLA 360

Qy 154 ----- 172
 Db 154 ----- 172

Qy 361 SEDSAVFCARRETTTGVRYVYAMDYWGQGTSTVTVSSAKTPKLGGDIVLTQSPALMSAS 420
 Db 361 SEDSAVFCARRETTTGVRYVYAMDYWGQGTSTVTVSSAKTPKLGGDIVLTQSPALMSAS 420

Qy 173 PQEKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVPAPHFRGSGSGTSYSLTI 232
 Db 421 PQEKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVPAPHFRGSGSGTSYSLTI 480

Qy 233 SCWEAEDAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLISEEDLNSHHHHH 291
 Db 481 SCWEAEDAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLISEEDLNSHHHHH 539

RESULT 2
 AAY50822
 ID AAY50822 standard; Protein; 554 AA.

XX AC AAY50822;
 XX DT 18-FEB-2000 (first entry)
 XX DE Fv-antibody construct containing antibody 9E10 epitope protein.
 XX KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
 XX KW diagnosis; therapy; disease.
 XX OS Synthetic.
 XX PN DE19819846-A1.
 XX XX 11-NOV-1999.

XX 05-MAY-1998; 98DE-1019846.
 PF 05-MAY-1998; 98DE-1019846.
 PR (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX Little M, Kipriyanov S;
 XX WPI; 2000-024472/03.
 DR N-PSDB; AAZ43431.
 XX Multivalent Fv-antibody constructs with at least four variable domains
 PT connected by 1, 2 and 3 peptide linkers
 PS Example 1; Fig 5; 14pp; German.
 XX This invention describes a novel multivalent Fv-antibody construct with
 CC at least four variable domains that are connected to one another by 1,
 CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
 CC and cytostatic activity. The multivalent Fv-antibody constructs are
 CC useful for the diagnosis and/or therapy of disease, especially viral,
 CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
 CC increased stability when in the form of a single chain dimer. This
 CC sequence represents a bivalent Fv antibody construct composed of the
 CC antibody 9E10 epitope in expression plasmid pDISC3x19-SL

XX Query Match 87.7%; Score 1346.5; DB 21; Length 554;
 PS Best Local Similarity 51.4%; Pred. No. 1.9e-79;
 XX Matches 285; Conservative 2; Mismatches 4; Indels 263; Gaps 3;

Qy 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMCKASGYTFTRYTHHWK 60
 Db 1 MKYLLPTAAAGLLLLAAQPAMAQVLOQSGAELARPGASVKMCKASGYTFTRYTHHWK 60

Qy 61 QPQGGLEWIGVINSRGYTNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120
 Db 61 QPQGGLEWIGVINSRGYTNQKFKDKATLTDDKSSSTAYMQLSSLTSEDSAVVYCAR 120

Qy 121 YYDDHSLDYWGQGTTLTVSSAKTPKL----- 148
 Db 121 YYDDHSLDYWGQGTTLTVSSAKTPKLGGDILLTQTPASLAVSLGORATISCKASQSV 180

Qy 149 ----- 148
 Db 149 ----- 148

Qy 181 YDGD SYLWYQIIPGPPKLLIYDASNLVSGIPPRFSGSGGTDFTLNHPVEKVDAA 240
 Db 149 ----- 148

Qy 241 HQQSTEDPWTGGGKLEIKRADAAGGPGSQVLOQSGAELVPGSSVKISCKASGY 300
 Db 149 ----- 153

Qy 301 AFSSYMNWVKORPGGLEWIGQIWPFGDGTNYNGKFKGKATLTADSSSTAYMQLSSLA 360
 Db 154 ----- 158

Qy 361 SEDSAVFCARRETTTGVRYVYAMDYWGQGTSTVTVSSAKTPKLGGDIVLTQSPALMSAS 420
 Db 159 DIVLTQSPALMSASPGKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVP 217

Qy 421 GDIVLTQSPALMSASPGKVTMTCSASSSVSYMNWYQKSGTSPKRWIYDTSKLASGVP 480
 Db 218 HFRGSGSGTSYSLTISGMEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLI 277

Qy 481 HFRGSGSGTSYSLTISGMEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTGSQKLI 540
 Db 278 ISEEDLNSHHHHH 291
 Db 541 ISEEDLNSHHHHH 554

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 12, 2003, 10:21:03 ; Search time 12 Seconds
(without alignments)
470.476 Million cell updates/sec

Title: US-09-424-705B-2

Perfect score: 1536
Sequence: 1 MYLLPTAAGLLLAQPA.....GSEQLISEEDLNHHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

T number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	872.5	56.8	239	10	US-09-808-037-6 Sequence 6, Appl1
2	858	55.9	240	10	US-09-976-787-28 Sequence 28, Appl1
3	858	55.9	240	10	US-09-865-198-27 Sequence 27, Appl1
4	850	55.3	238	10	US-09-976-787-29 Sequence 29, Appl1
5	850	55.3	238	10	US-09-865-198-28 Sequence 28, Appl1
6	817.5	53.2	288	10	US-09-818-247-22 Sequence 22, Appl1
7	813.5	53.0	260	10	US-09-811-737-16 Sequence 16, Appl1
8	809.5	52.7	260	10	US-09-811-737-17 Sequence 17, Appl1
9	763.5	49.7	669	9	US-09-807-721-2 Sequence 2, Appl1
10	751	48.9	244	10	US-09-940-391-1 Sequence 1, Appl1
11	724	47.1	249	10	US-09-984-186-18 Sequence 18, Appl1
12	719	46.8	253	10	US-09-811-737-18 Sequence 18, Appl1
13	710	46.2	253	10	US-09-924-099-10 Sequence 10, Appl1
14	707	46.0	255	10	US-09-811-737-15 Sequence 15, Appl1
15	706.5	46.0	267	10	US-09-766-543-10 Sequence 10, Appl1
16	696.5	45.3	245	9	US-09-991-470-27 Sequence 27, Appl1
17	690.5	45.0	535	9	US-09-968-851-38 Sequence 38, Appl1
18	689	44.9	252	9	US-09-887-853-4 Sequence 4, Appl1
19	682.5	44.4	237	10	US-09-924-099-9 Sequence 9, Appl1

20	673	43.8	250	9	US-09-887-853-2 Sequence 2, Appl1
21	667.5	43.5	270	10	US-09-976-118-2 Sequence 2, Appl1
22	662.5	43.1	276	10	US-09-766-543-12 Sequence 12, Appl1
23	656.5	42.7	240	9	US-09-968-561A-2 Sequence 2, Appl1
24	656.5	42.7	240	10	US-09-192-854-2 Sequence 2, Appl1
25	650.5	42.4	262	10	US-09-811-737-19 Sequence 19, Appl1
26	646.5	42.1	268	10	US-09-976-118-1 Sequence 1, Appl1
27	645.5	42.0	269	12	US-10-027-770-2 Sequence 1, Appl1
28	640.5	41.7	269	12	US-10-027-770-5 Sequence 5, Appl1
29	637.5	41.5	248	10	US-09-920-171-22 Sequence 22, Appl1
30	635.5	41.4	248	10	US-09-920-171-23 Sequence 23, Appl1
31	618.5	40.3	241	1	US-08-779-457-50 Sequence 50, Appl1
32	617	40.2	243	9	US-09-887-853-6 Sequence 6, Appl1
33	615.5	40.1	249	1	US-08-779-457-48 Sequence 48, Appl1
34	609	39.6	310	12	US-10-052-798-11 Sequence 11, Appl1
35	606.5	39.5	269	10	US-09-888-721-36 Sequence 36, Appl1
36	606.5	39.5	282	10	US-09-888-721-38 Sequence 38, Appl1
37	606.5	39.5	287	10	US-09-888-721-40 Sequence 40, Appl1
38	606.5	39.5	291	10	US-09-888-721-44 Sequence 44, Appl1
39	606.5	39.5	296	10	US-08-888-721-42 Sequence 42, Appl1
40	603	39.3	250	1	US-08-779-457-49 Sequence 49, Appl1
41	599	39.0	249	10	US-09-730-374-3 Sequence 3, Appl1
42	598	38.9	245	12	US-10-039-785-46 Sequence 46, Appl1
43	597	38.9	381	10	US-09-822-698A-5 Sequence 5, Appl1
44	582	37.9	245	12	US-10-039-785-42 Sequence 42, Appl1
45	582	37.9	245	12	US-10-039-785-43 Sequence 43, Appl1

ALIGNMENTS

RESULT 1
US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US2002005231A1
; GENERAL INFORMATION:
; APPLICANT: HANAN, Elia
; APPLICANT: SOLOMON, Beke
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 1999-09-03
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

Query Match 56.8%; Score 872.5; DB 10; Length 239;
Best Local Similarity 71.4%; Pred. No. 7.8e-42;
Matches 177; Conservative 13; Mismatches 41; Indels 17; Gaps 3;
QY 23 QVQLQSGAEELRPASVSMKSCASGYTFRYTMHWKORPGGLEWIGYINRSRYTNY 82
DB 1 QVQLQSGAEELRPASVSMKSCASGYTFRYTMHWKORPGGLEWIGYINRSRYTNY 60
QY 83 NQKFKDKATLTDDKSSSTAYMQLSLTSEDAVYVCARYDDHYSLDYWGQGLTLTVSSA 142
DB 61 NQKFKDKATLTDDKSSSTAYMQLSLTSEDAVYVCARYDDHYSLDYWGQGLTLTVSSA 118
QY 143 KTTPKLEEFSEFSAFY-----DIVLTQSPAIMASPEKTYMTTCSSASSVSYMMWYQO 195
DB 119 -----GGGGGGVGGGGGGGDIETLQSPAIMASPEKTYMTTCSSASSVSYMMWYQO 170

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Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2003, 10:19:49 ; Search time 15 Seconds

(without alignments)
570.805 Million cell updates/sec

Title: US-09-424-705b-2

Perfect score: 1536
Sequence: 1 MKYLLPTAAGLLILAAOPA.....GSEQKLSIEDINSHHHH 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

TC: number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1010.5	65.8	281	4	US-09-423-439-44
2	974	63.4	246	1	US-08-469-486-57
3	974	63.4	246	2	US-08-469-658-57
4	963.5	62.7	239	4	US-08-279-772A-8
5	963.5	62.7	239	4	US-08-902-486-11
6	957.5	62.3	599	1	US-08-463-163-3
7	947	61.7	288	4	US-09-423-439-38
8	928.5	60.4	270	2	US-08-652-507-2
9	919	59.8	244	2	US-08-553-497A-20
10	912	59.4	267	4	US-09-485-737B-2
11	908	59.1	246	2	US-08-553-497A-24
12	905	58.9	244	2	US-08-553-497A-22
13	901	58.7	242	2	US-08-553-497A-26
14	898	58.5	553	4	US-08-661-052-16
15	898	58.5	553	4	US-09-188-082-16
16	898	58.5	553	4	US-09-364-088-16
17	898	58.5	553	4	US-09-102-716-16
18	889.5	57.9	271	2	US-08-894-922A-10
19	886	57.7	242	2	US-08-553-497A-28
20	874.5	56.9	273	2	US-08-403-853-18
21	852	55.5	255	4	US-09-553-498-8
22	852	55.5	255	4	US-09-618-869-8
23	833.5	54.3	284	3	US-09-184-658-40
24	828.5	53.9	666	4	US-09-423-439-51
25	815.5	53.1	230	4	US-09-485-737B-102
26	814.5	53.0	240	4	US-09-485-737B-91
27	813	52.9	235	4	US-09-485-737B-93

28	808	52.6	541	4	US-09-485-737B-85	Sequence 85, Appl
29	796	51.8	223	2	US-08-190-199A-63	Sequence 63, Appl
30	788.5	51.3	252	2	US-08-894-922A-14	Sequence 14, Appl
31	788	51.3	269	2	US-08-428-257A-72	Sequence 72, Appl
32	788	51.3	269	2	US-08-491-988-3	Sequence 3, Appl
33	788	51.3	402	2	US-08-491-988-9	Sequence 9, Appl
34	788	51.3	415	2	US-08-491-988-7	Sequence 7, Appl
35	788	51.3	435	2	US-08-491-988-5	Sequence 5, Appl
36	783.5	51.0	236	2	US-08-190-199A-65	Sequence 65, Appl
37	781	50.8	711	4	US-09-485-737B-90	Sequence 90, Appl
38	776.5	50.6	240	2	US-08-800-198-8	Sequence 8, Appl
39	776.5	50.6	240	2	US-09-296-595-8	Sequence 8, Appl
40	773.5	50.4	222	2	US-08-190-199A-67	Sequence 67, Appl
41	771.5	50.2	240	2	US-08-956-047-25	Sequence 25, Appl
42	770.5	50.2	269	4	US-08-646-265A-109	Sequence 109, Appl
43	765	49.8	673	4	US-09-423-439-32	Sequence 32, Appl
44	761	49.5	235	2	US-08-190-199A-61	Sequence 61, Appl
45	752	49.0	553	2	US-08-263-911-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-423-439-44
; Sequence 44, Application US/09423439
; Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKLEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423 439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44
Query Match 65.8%; Score 1010.5; DB 4; Length 281;
Best Local Similarity 70.4%; Pred. No. 3.3e-70;
Matches 205; Conservative 20; Mismatches 55; Indels 11; Gaps 3;
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Db 121 LIYAGYLANDYWGQGTTSVAVSGGGGS--GGGGSGGGGSIQVLTQSPAINMSAPGKVTI 178
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Db 239 AATYQCQSSNPFTGSGTKLEIKR-----EQKLISEEDLNHHHHH 281

RESULT 2
US-08-469-486-57
; Sequence 57, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-486-57

Query Match 63.4%; Score 974; DB 1; Length 246;
Best Local Similarity 74.5%; Pred. No. 1.8e-67;
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QY 23 QVLOQSGAELARPGASVKMSCKASGYTFTRYTMHWVKORPGQGLEWIGYINPSRGYTN 82
Db 1 QVKLQSGAELVKPGASVKMSCKASGYTFASYWINWVKORPGQGLEWIGHIYVRSITKY 60
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Db 121 G-----GGGS-----DIELTQSPAILSPGKVTMTCRASSSVSYMMHWYQKPGSSP 168
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Db 229 EIKRA-----AAEQKLISEEDLN 246

RESULT 3
US-08-469-658-57
; Sequence 57, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-658-57

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:55:54 ; Search time 455.268 Seconds

(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Mask size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO9957150.
ACCESSION AX011208
VERSION AX011208.1 GI:9997788
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1653)
AUTHORS Kipriyanov,S. and Little,M.
TITLE Multivalent antibody constructs
JOURNAL Patent: WO 9957150-A 3 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
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DEFINITION Human DNA sequence from clone RP3-481C9 on chromosome 6q25.1-26,
complete sequence.
ACCESSION AL133510
VERSION AL133510.13 GI:13160149
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ACCESSION AX011206
VERSION AX011206.1 GI:9997786
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1698)
AUTHORS Kipriyanov,S. and Little,M.
TITLE Multivalent antibody constructs
JOURNAL Patent: WO 9957150-A 1 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
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LOCUS AL133510 122680 bp DNA linear PRI 01-MAR-2001
DEFINITION Human DNA sequence from clone RP3-481C9 on chromosome 6q25.1-26,
complete sequence.
ACCESSION AL133510
VERSION AL133510.13 GI:13160149
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BASE COUNT 433 a 434 c 450 g 381 t
ORIGIN

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 768 Seconds
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506.109 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 73	15	62.5	938	12	BF162175	BF162175 601770649
C 74	15	62.5	997	17	CNS0706F	AL440077 T3 end of
C 75	15	62.5	1044	12	BF578042	BF578042 602091888
C 76	15	62.5	1103	14	BM920389	BM920389 AGENCOURT
C 77	15	62.5	1313	17	BH860804	BH860804 ORNL269.P
C 78	15	62.5	1355	11	AK008855	AK008855 Mus muscu
C 79	15	58.3	105	9	AA588295	AA588295 mm51a01.s

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80      14 58.3 117 17 AQ490507
81      14 58.3 132 17 AQ097748
82      14 58.3 142 13 BM287615
83      14 58.3 150 17 AQ470161
84      14 58.3 152 17 BH052149
85      14 58.3 157 12 BF335466
86      14 58.3 184 9 A1180583
87      14 58.3 200 10 AW733266
88      14 58.3 230 9 A1616213
89      14 58.3 241 9 AV014889
90      14 58.3 244 17 BH667684
91      14 58.3 250 9 AV013654
92      14 58.3 250 17 AQ097325
93      14 58.3 256 17 AQ097325
94      14 58.3 257 17 BH175913
95      14 58.3 265 9 AV222455
96      14 58.3 269 10 AW854223
97      14 58.3 270 9 AA322799
98      14 58.3 271 14 BQ247264
99      14 58.3 282 17 BH870924
100     14 58.3 284 13 B1436565

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ALIGNMENTS

```

RESULT 1
AI632464/c      278 bp mRNA linear EST 17-DEC-1999
LOCUS          wb09d06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2305163 3'
DEFINITION     similar to contains Alu repetitive element, mRNA sequence.
ACCESSION      AI632464
VERSION        AI632464.1 GI:4683794
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 278)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 381 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="(vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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FEATURES

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source
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="(vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

```

BASE COUNT      67 a      75 c      57 g      79 t
ORIGIN
Query Match      70.8%; Score 17; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 AGTCAAGGCTGTAATGA 19
      |||
Db      72 AGTCAAGGCTGTAATGA 56

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RESULT 2

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AW594601/c      278 bp mRNA linear EST 22-MAR-2000
LOCUS          hg67d06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2950667 3'
DEFINITION     similar to contains Alu repetitive element, mRNA sequence.
ACCESSION      AW594601
VERSION        AW594601.1 GI:7281951
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 278)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="(vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

FEATURES

```

source
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="(vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

FEATURES

```

source
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="(vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

```

BASE COUNT      67 a      75 c      57 g      79 t
ORIGIN
Query Match      70.8%; Score 17; DB 10; Length 278;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      3 AGTCAAGGCTGTAATGA 19
      |||
Db      72 AGTCAAGGCTGTAATGA 56

```

RESULT 3

```

BB634155
LOCUS          BB634155      657 bp mRNA linear EST 26-OCT-2001

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 96.7317 Seconds
(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-7

Perfect score: 24
Sequence: 1 gtagcagacgctgaatgcatc 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wc size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	AAV73336	Mouse OKT3 variant
2	24	100.0	898	AAV73335	Mouse OKT3 variant
3	24	100.0	1653	AAZ43432	Fv-antibody constr
4	24	100.0	1698	AAZ43431	Fv-antibody constr
5	24	100.0	1794	AAV73337	Mouse bispecific a
6	16	66.7	346	AA537402	Novel human diagno
7	16	66.7	487	AA181103	Human polynucleoti
8	16	66.7	13024	AA104739	Human reproductive
9	16	66.7	13024	AB197644	Human testicular a

10	16	66.7	22651	22	AAK78202	Human immune/haema
11	16	66.7	28180	22	AAK68939	Human immune/haema
12	15	62.5	17	22	AAAF57365	Murine Cdc25A intr
13	15	62.5	261	21	AAC27376	Human secreted pro
14	15	62.5	431	23	ABV16978	Human prostate exp
15	15	62.5	441	22	AAK75439	Human immune/haema
16	15	62.5	441	22	AAK75440	Human immune/haema
17	15	62.5	478	23	AAV46773	Human prostate exp
18	15	62.5	545	18	AAK30815	Human immune/haema
19	15	62.5	654	19	AAAT9657	Streptococcus pneu
20	15	62.5	1428	21	AAA05441	DNA encoding a S.
21	15	62.5	2690	18	AAAT59990	Streptococcus pneu
22	15	62.5	12665	19	AAV52267	Glucose repressor
23	15	62.5	21429	22	AAAF57362	Streptococcus pneu
24	15	62.5	30175	24	AAAD32742	Murine Cdc25A comp
25	15	62.5	59060	22	AAK85994	Human drug metabol
26	15	109906	24	24	ABK94411	Human immune/haema
27	14	58.3	225	24	ABK91407	DNA encoding endot
28	14	58.3	354	21	AAAF6037	Staphylococcus epi
29	14	58.3	587	21	AAAF08479	Pseudomonas ppqf g
30	14	58.3	608	21	AAAD00428	Fusarium venenatum
31	14	58.3	680	22	AAAD17148	Human MINT10 DNA c
32	14	58.3	861	24	ABK78815	Human ion channel-
33	14	58.3	954	24	ABK78815	Bacillus clausii g
34	14	58.3	1161	21	AAK91412	Staphylococcus epi
35	14	58.3	1392	21	AAK37583	Arabidopsis thalia
36	14	58.3	1392	23	AAAS9712	Propionibacterium
37	14	58.3	1393	21	AAAC50697	Arabidopsis thalia
38	14	58.3	1443	22	AAH68451	C glutamicum codin
39	14	58.3	1446	14	AAQ52852	Theonine synthase
40	14	58.3	1566	22	AAAF71840	Corynebacterium gl
41	14	58.3	1708	22	AAAF60145	Human polynucleoti
42	14	58.3	1760	21	AAAC4674	Zea mays DNA fragm
43	14	58.3	1981	22	AAI66558	Human bromine grou
44	14	58.3	2007	22	AAI58359	Human polynucleoti
45	14	58.3	2224	24	AAH02744	Human amyloid prec
46	14	58.3	2417	21	AAH06950	Human immunogenic
47	14	58.3	2417	22	AAAS63772	Human prostate cDN
48	14	58.3	2417	22	AAH93679	Human prostate-spe
49	14	58.3	2417	22	AAH82493	Human prostate-spe
50	14	58.3	2417	22	AAH02744	Prostate tumour an
51	14	58.3	2417	22	AAAF6950	Human P714P invent
52	14	58.3	2417	24	AAV52247	Human P714P CDNA s
53	14	58.3	2560	19	AAV52247	Streptococcus pneu
54	14	58.3	2742	22	AAH15707	Human CDNA sequenc
55	14	58.3	2976	22	AAK53269	Human polynucleoti
56	14	58.3	3096	22	ABK21462	Human nervous syst
57	14	58.3	3146	9	AAH81713	Clone contg. thrc
58	14	58.3	3220	22	AAK54856	CDNA encoding nove
59	14	58.3	3276	22	AAK52285	Human polynucleoti
60	14	58.3	3440	23	ABV23315	Human prostate exp
61	14	58.3	3440	23	ABV22159	Human prostate exp
62	14	58.3	3440	23	ABV27134	Human prostate exp
63	14	58.3	3440	23	ABV27998	Human prostate exp
64	14	58.3	3520	22	AAH54185	S. epidermidis gen
65	14	58.3	3585	21	AAAF97456	Human RalGDS (hral
66	14	58.3	3674	22	AAK64034	Human prostate cDN
67	14	58.3	3674	22	AAH93862	P714P extended CDN
68	14	58.3	3674	24	ABL95405	Human P714P CDNA s
69	14	58.3	3767	23	ABL17754	Drosophila melanog
70	14	58.3	5009	13	AAQ21412	Carbonic anhydrase
71	14	58.3	10425	23	ABL25360	Drosophila melanog
72	14	58.3	14637	22	AAK71065	Human genomic DNA
73	14	58.3	16176	22	AAK71065	Human immune/haema
74	14	58.3	17700	22	AAK68945	Human immune/haema
75	14	58.3	28470	22	AAK71445	Human immune/haema
76	14	58.3	29255	23	AAAS9516	Propionibacterium
77	14	58.3	37716	23	AAAS9553	Propionibacterium
78	14	58.3	56516	20	AAZ00870	Pgi genomic coding
79	14	58.3	56520	20	AAZ01022	Wild type Pgi codi
80	14	58.3	34980	22	AAH68531	C glutamicum codin
81	14	58.3	236589	24	ABA90521	Genomic sequence o
82	13	54.2	65	24	ABN52848	Mouse spliced tran

83 13 54.2 73 16 AAT25114 Human gene signatu
 84 13 54.2 96 21 AAC12679 Human secreted pro
 85 13 54.2 156 19 AAV33544 Clone 132750 cDNA
 86 13 54.2 183 23 AAS50445 Staphylococcus aur
 87 13 54.2 201 24 AAD33411 Human organic anio
 88 13 54.2 217 20 AAH86987 Human single nucle
 89 13 54.2 227 18 AAX83372 Breast cancer tumo
 90 13 54.2 227 19 AAV68911 DNA molecule encod
 91 13 54.2 227 21 AAC80895 Human breast tumou
 92 13 54.2 227 24 ABK46785 Human breast tumou
 93 13 54.2 227 24 AAS99741 Breast tumour-spec
 94 13 54.2 229 20 AAV86596 EST clone BG48. H
 95 13 54.2 251 19 AAX11171 Human biallelic po
 96 13 54.2 251 19 AAX11172 Human biallelic po
 97 13 54.2 279 23 ABV57833 Human prostate exp
 98 13 54.2 289 23 AAS49767 Staphylococcus aur
 99 13 54.2 289 23 AAS49786 Staphylococcus aur
 100 13 54.2 289 23 AAS49792 Staphylococcus aur

ALIGNMENTS

RESULT 1
 AAV73336
 ID AAV73336 standard; DNA; 24 BP.
 AC AAV73336;
 DT 26-FEB-1999 (first entry)
 XX Mouse OKT3 variant antibody primer SK1 DNA.
 DE OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; primer; ss.
 XX Synthetic.
 OS Mus sp.
 PN DE19721700-Cl.
 PD 19-NOV-1998.
 XX 23-MAY-1997; 97DE-1021700.
 PF 23-MAY-1997; 97DE-1021700.
 PR 23-MAY-1997; 97DE-1021700.
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI; 1998-596150/51.
 DR Monoclonal antibody OKT3 with point-mutation - where cysteine is
 PT replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 XX Claim 7; Column 3; 8pp; German.
 PS This sequence is a primer used in the construction of a monoclonal
 CC antibody (MAb) derived from OKT3 with a point-mutation where Cys at
 CC position H100A is replaced with another polar amino acid, in this example
 CC Ser. The MAb is used in lowering or eliminating the transplant rejection
 CC in an organ recipient and for diagnostic methods for tumours and tumour
 CC therapy.
 XX Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;
 SQ Query Match 100.0%; Score 24; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTAGTCAAGGCTGTAATGATCATC 24

Db 1 GTAGTCAAGGCTGTAATGATCATC 24
 RESULT 2
 AAV73335/c
 ID AAV73335 standard; DNA; 898 BP.
 XX AAV73335;
 AC AAV73335;
 DT 26-FEB-1999 (first entry)
 XX Mouse OKT3 variant antibody DNA.
 DE OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; ss.
 XX Mus sp.
 OS Synthetic.
 PN DE19721700-Cl.
 PD 19-NOV-1998.
 XX 23-MAY-1997; 97DE-1021700.
 PF 23-MAY-1997; 97DE-1021700.
 PR 23-MAY-1997; 97DE-1021700.
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI; 1998-596150/51.
 DR P-PSDB; AAW82316.
 DR Monoclonal antibody OKT3 with point-mutation - where cysteine is
 PT replaced by another polar amino acid, useful for controlling
 PT transplant rejection, and in tumour diagnostics and therapy
 XX Claim 3; Fig 2; 8pp; German.
 PS This sequence encodes a monoclonal antibody (MAb) derived from OKT3 with
 CC a point-mutation where Cys at position H100A is replaced with another
 CC polar amino acid, in this example Ser. The MAb is used in lowering or
 CC eliminating the transplant rejection in an organ recipient, and for
 CC diagnostic methods for tumours and tumour therapy.
 XX Sequence 898 BP; 245 A; 236 C; 217 G; 200 T; 0 other;
 SQ Query Match 100.0%; Score 24; DB 19; Length 898;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTAGTCAAGGCTGTAATGATCATC 24
 Db 417 GTAGTCAAGGCTGTAATGATCATC 394
 RESULT 3
 AAZ43432/c
 ID AAZ43432 standard; DNA; 1653 BP.
 XX AAZ43432;
 AC AAZ43432;
 DT 18-FEB-2000 (first entry)
 XX Fv-antibody construct containing antibody 9E10 epitope DNA.
 DE Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
 KW diagnosis; therapy; disease; ss.
 XX Synthetic.
 OS

PN DE19819846-A1.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1998; 98DE-1019846.
XX
PR 05-MAY-1998; 98DE-1019846.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Little M, Kipriyanov S;
XX
DR WPI; 2000-024472/03.
XX
PT Multivalent Fv-antibody constructs with at least four variable domains
XX connected by 1, 2 and 3 peptide linkers -
PS Example 1; Fig 6; 14pp; German.
XX
CC This invention describes a novel multivalent Fv-antibody construct with
CC at least four variable domains that are connected to one another by 1,
CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
CC and cytostatic activity. The multivalent Fv-antibody constructs are
CC useful for the diagnosis and/or therapy of disease, especially viral,
CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
CC increased stability when in the form of a single chain dimer. This
CC sequence encodes a trivalent Fv antibody construct composed of the
CC antibody 9E10 epitope in expression plasmid pDISC3x19-SL
XX
SQ Sequence 1653 BP; 432 A; 429 C; 424 G; 368 T; 0 other;
XX
Query Match 100.0%; Score 24; DB 21; Length 1653;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGTCAAGGCTGTAATGATCATC 24
DB 417 GTAGTCAAGGCTGTAATGATCATC 394
XX
RESULT 4
AA243431/c
ID AA243431 standard; DNA; 1698 BP.
XX
AC AA243431;
XX
DT 18-FEB-2000 (first entry)
XX
D Fv-antibody construct containing antibody 9E10 epitope DNA.
XX
KM Multivalent; Fv-antibody; antiviral, antibacterial; cytostatic;
XX diagnosis; therapy; disease; ss.
XX
OS Synthetic.
XX
PN DE19819846-A1.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1998; 98DE-1019846.
XX
PR 05-MAY-1998; 98DE-1019846.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Little M, Kipriyanov S;
XX
DR WPI; 2000-024472/03.
XX
PT Multivalent Fv-antibody constructs with at least four variable domains
XX connected by 1, 2 and 3 peptide linkers -

PS Example 1; Fig 5; 14pp; German.
XX
CC This invention describes a novel multivalent Fv-antibody construct with
CC at least four variable domains that are connected to one another by 1,
CC 2 and 3 peptide linkers. The construct has antiviral, antibacterial
CC and cytostatic activity. The multivalent Fv-antibody constructs are
CC useful for the diagnosis and/or therapy of disease, especially viral,
CC bacterial or tumor diseases. The multivalent Fv-antibody constructs have
CC increased stability when in the form of a single chain dimer. This
CC sequence encodes a bivalent Fv antibody construct composed of the
CC antibody 9E10 epitope in expression plasmid pDISC3x19-LL
XX
SQ Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 other;
XX
Query Match 100.0%; Score 24; DB 21; Length 1698;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAGTCAAGGCTGTAATGATCATC 24
DB 417 GTAGTCAAGGCTGTAATGATCATC 394
XX
RESULT 5
AAV73337/c
ID AAV73337 standard; DNA; 1794 BP.
XX
AC AAV73337;
XX
DT 26-FEB-1999 (first entry)
XX
DE Mouse bispecific antibody construct variant OKT3/anti-CD19 DNA.
XX
KM OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;
XX organ recipient; diagnosis; tumour; therapy; antibody; anti-CD19;
XX anti-CD3; ss.
XX
OS Mus sp.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 28..894
FT /*tag= a
FT /product= "mutant OKT3 with anti-CD19 insert"
FT CDS 922..1788
FT /*tag= b
FT /product= "mutant OKT3 with anti-CD3 insert"
XX
PN DE19721700-C1.
XX
PD 19-NOV-1998.
XX
PF 23-MAY-1997; 97DE-1021700.
XX
PR 23-MAY-1997; 97DE-1021700.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Kipriyanov S, Little M, Moldenhauer G;
XX
DR WPI; 1998-596150/51.
XX
DR P-PSDB; AAW82317, AAW82482.
XX
PT Monoclonal antibody OKT3 with point-mutation - where cysteine is
XX replaced by another polar amino acid, useful for controlling
XX transplant rejection, and in tumour diagnostics and therapy
XX
PS Disclosure; Fig 3; 8pp; German.
XX
CC This sequence encodes a monoclonal antibody (MAb) diabody derived from
CC OKT3 with a point-mutation where Cys at position H100A is replaced with
CC another polar amino acid, in this example Ser. The diabody encodes two
CC OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3

CC activity. The MAb is used in lowering or eliminating the transplant
CC rejection in an organ recipient and for diagnostic methods for tumours
CC and tumour therapy.

XX
SQ Sequence 1794 BP; 480 A; 468 C; 450 G; 396 T; 0 other;
Query Match 100.0%; Score 24; DB 19; Length 1794;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAGTCAAGGCTGTAATGATC 24
|||||
Db 417 GTAGTCAAGGCTGTAATGATC 394
|||||

RESULT 6
AAS37402
ID AAS37402 standard; cDNA; 346 BP.
XX
AC AAS37402;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #460.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US07787.
XX
PR 09-MAR-2000; 2000US-0188609.
XX
PA (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
WPI; 2001-530177/58.
XX
DR New polynucleotides and polypeptides, useful for diagnosis and
XX treatment of breast, lung and colon cancer -
XX
PS Claim 1; Page 712; 1193pp; English.
XX
CC The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention.
XX
SQ Sequence 346 BP; 112 A; 67 C; 87 G; 79 T; 1 other;
Query Match 66.7%; Score 16; DB 22; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATGA 19
|||||
Db 320 GTCAAGGCTGTAATGA 335
|||||

RESULT 7
AAI81103/c
ID AAI81103 standard; cDNA; 487 BP.
XX
AC AAI81103;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1163.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
WPI; 2001-514838/56.
XX
DR P-PSDB; AAO01172.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
PS Claim 1; SEQ ID NO 1163; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 487 BP; 125 A; 128 C; 102 G; 130 T; 2 other;
Query Match 66.7%; Score 16; DB 22; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATGA 19
|||||
Db 412 GTCAAGGCTGTAATGA 397
|||||

RESULT 8
AAL04739
ID AAL04739 standard; DNA; 13024 BP.
XX
AC AAL04739;
XX
DT 21-NOV-2001 (first entry)
XX

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 18.7317 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-7

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Mask size: 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

Database : Published Applications_NA.*

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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15	62.5	30175	12	US-10-163-381-3	Sequence 3, Appl1
C 3	14	58.3	341	10	US-09-783-590-10253	Sequence 10253, A
C 4	14	58.3	517	10	US-09-783-590-358	Sequence 358, App
C 5	14	58.3	861	10	US-09-974-300-6106	Sequence 6106, App
C 6	14	58.3	1167	9	US-09-938-842A-1133	Sequence 1133, Ap
C 7	14	58.3	1443	9	US-09-738-626-3486	Sequence 3486, App
C 8	14	58.3	2417	9	US-09-232-880-334	Sequence 334, App
C 9	14	58.3	2417	9	US-10-012-896-334	Sequence 334, App
C 10	14	58.3	2417	9	US-09-895-793-334	Sequence 334, App
C 11	14	58.3	2417	9	US-09-895-814-334	Sequence 334, App
C 12	14	58.3	2417	10	US-09-759-143-334	Sequence 334, App
C 13	14	58.3	2417	10	US-09-780-669-334	Sequence 334, App
C 14	14	58.3	2417	10	US-09-822-827-334	Sequence 334, App
C 15	14	58.3	2709	9	US-09-922-199A-3	Sequence 3, Appl1
C 16	14	58.3	3674	9	US-10-012-896-698	Sequence 698, App
C 17	14	58.3	3674	9	US-09-895-793-698	Sequence 698, App
C 18	14	58.3	3674	9	US-09-895-814-698	Sequence 698, App
C 19	14	58.3	3674	10	US-09-759-143-698	Sequence 698, App

20	14	58.3	3674	10	US-09-780-669-698	Sequence 698, App
21	14	58.3	3674	10	US-09-822-827-698	Sequence 698, App
22	14	58.3	3691	9	US-09-922-199A-1	Sequence 1, Appl1
23	14	58.3	56516	9	US-09-853-526-1	Sequence 1, Appl1
24	14	58.3	56516	10	US-09-901-484A-1	Sequence 1, Appl1
25	14	58.3	56520	9	US-09-853-526-179	Sequence 179, App
26	14	58.3	56520	10	US-09-901-484A-179	Sequence 179, App
27	13	54.2	183	10	US-09-815-242-3022	Sequence 3022, App
28	13	54.2	201	10	US-09-925-731-11	Sequence 11, Appl1
29	13	54.2	227	9	US-09-924-400-183	Sequence 183, App
30	13	54.2	227	10	US-09-810-936-183	Sequence 183, App
31	13	54.2	227	10	US-09-429-755-183	Sequence 183, App
32	13	54.2	267	10	US-09-878-574-11257	Sequence 11257, A
33	13	54.2	271	10	US-09-878-574-11153	Sequence 11153, A
34	13	54.2	271	10	US-09-878-574-14243	Sequence 14243, A
35	13	54.2	282	10	US-09-983-965-3146	Sequence 3146, App
36	13	54.2	289	10	US-09-815-242-2344	Sequence 2344, App
37	13	54.2	289	10	US-09-815-242-2363	Sequence 2363, App
38	13	54.2	289	10	US-09-815-242-2369	Sequence 2369, App
39	13	54.2	289	10	US-09-815-242-2327	Sequence 3227, App
40	13	54.2	324	10	US-09-764-877-3392	Sequence 3392, App
41	13	54.2	339	10	US-09-764-877-676	Sequence 676, App
42	13	54.2	371	10	US-09-867-701-10550	Sequence 10550, A
43	13	54.2	398	10	US-09-983-965-184	Sequence 184, App
44	13	54.2	401	9	US-09-946-807-478	Sequence 478, App
45	13	54.2	401	10	US-09-795-668-478	Sequence 478, App
46	13	54.2	401	10	US-09-795-668-478	Sequence 478, App
47	13	54.2	405	9	US-09-796-692-2980	Sequence 2980, App
48	13	54.2	424	10	US-09-867-701-8930	Sequence 8930, App
49	13	54.2	432	10	US-09-960-352-2913	Sequence 2913, App
50	13	54.2	436	10	US-09-983-965-458	Sequence 458, App
51	13	54.2	446	10	US-09-864-761-1959	Sequence 1959, App
52	13	54.2	491	10	US-09-783-590-6297	Sequence 6297, App
53	13	54.2	521	10	US-09-864-761-8459	Sequence 8459, App
54	13	54.2	552	10	US-09-974-300-1433	Sequence 1433, App
55	13	54.2	572	10	US-09-864-761-14498	Sequence 14498, A
56	13	54.2	602	9	US-09-796-692-8538	Sequence 8538, App
57	13	54.2	699	9	US-09-738-626-921	Sequence 921, App
58	13	54.2	908	9	US-09-866-570A-23	Sequence 23, Appl1
59	13	54.2	908	10	US-09-866-572A-23	Sequence 23, Appl1
60	13	54.2	927	10	US-09-729-674-75	Sequence 75, Appl1
61	13	54.2	948	10	US-09-886-055-126	Sequence 126, App
62	13	54.2	1269	10	US-09-771-161A-21	Sequence 21, Appl1
63	13	54.2	1275	9	US-09-938-842A-1977	Sequence 1977, App
64	13	54.2	1586	10	US-09-870-962-11	Sequence 11, Appl1
65	13	54.2	1827	10	US-09-925-302-270	Sequence 270, App
66	13	54.2	1885	10	US-09-764-869-2417	Sequence 2417, App
67	13	54.2	1885	10	US-09-764-869-2419	Sequence 2419, App
68	13	54.2	2000	9	US-09-938-842A-4443	Sequence 4443, App
69	13	54.2	2010	10	US-09-878-756-3	Sequence 3, Appl1
70	13	54.2	2257	10	US-09-972-912-42	Sequence 42, Appl1
71	13	54.2	2448	10	US-09-967-768A-187	Sequence 187, App
72	13	54.2	2632	9	US-10-108-605-36	Sequence 36, Appl1
73	13	54.2	2920	10	US-09-956-004-10	Sequence 10, Appl1
74	13	54.2	6231	10	US-09-925-301-536	Sequence 536, App
75	13	54.2	6310	10	US-09-764-865-183	Sequence 183, App
76	13	54.2	6311	10	US-09-764-865-183	Sequence 183, App
77	13	54.2	8472	9	US-09-764-868-1306	Sequence 1306, App
78	13	54.2	8472	9	US-09-764-868-1307	Sequence 1307, App
79	13	54.2	11177	10	US-09-764-878-221	Sequence 221, App
80	13	54.2	1587	10	US-09-764-877-2134	Sequence 2134, App
81	13	54.2	26928	10	US-09-880-107-2278	Sequence 2278, App
82	13	54.2	31124	12	US-10-063-763-12	Sequence 12, Appl1
83	13	54.2	31730	10	US-09-764-877-3310	Sequence 3310, App
84	13	54.2	127197	9	US-09-754-853A-1	Sequence 1, Appl1
85	13	54.2	203554	10	US-09-820-905-3	Sequence 3, Appl1
86	12	50.0	102	10	US-09-864-761-21661	Sequence 21661, A
87	12	50.0	148	10	US-09-960-332-5126	Sequence 5126, A
88	12	50.0	154	10	US-09-864-761-33750	Sequence 33750, A
89	12	50.0	171	10	US-09-983-965-2164	Sequence 2164, App
90	12	50.0	217	10	US-09-867-550-967	Sequence 967, App
91	12	50.0	249	10	US-09-563-817-84	Sequence 84, Appl1
92	12	50.0	270	10	US-09-867-701-7646	Sequence 7646, App

C 93 12 50.0 277 10 US-09-878-574-15241, A
C 94 12 50.0 292 10 US-09-917-800A-1264
C 95 12 50.0 333 10 US-09-815-242-9155
C 96 12 50.0 340 10 US-09-880-107-862
C 97 12 50.0 343 10 US-09-764-869-272
C 98 12 50.0 345 10 US-09-974-300-8167
C 99 12 50.0 349 10 US-09-878-574-12
C 100 12 50.0 363 10 US-09-770-791-470

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Matches 15; Conservative 0; Mismatches 0;

Qy 5 TCAAGGCTGTAATGA 19
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Db 10418 TCAAGGCTGTAATGA 10404

ALIGNMENTS

RESULT 1

US-09-738-878-3/c
; Sequence 3, Application US/09738878
; Patent No. US2002022254A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000744

; CURRENT APPLICATION NUMBER: US/09/738, 878

; CURRENT FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 30175

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(30175)

; OTHER INFORMATION: n = A,T,C or G

US-09-738-878-3

Query Match 62.5%; Score 15; DB 10; Length 30175;
Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

Qy 5 TCAAGGCTGTAATGA 19
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Db 10418 TCAAGGCTGTAATGA 10404

RESULT 2

US-10-163-381-3/c
; Sequence 3, Application US/10163381
; Patent No. US20020151015A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL000744CON

; CURRENT APPLICATION NUMBER: US/10/163,381

; CURRENT FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: 60/221,509

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/738, 878

; PRIOR FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 30175

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(30175)

; OTHER INFORMATION: n = A,T,C or G

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	62.5	2690	4	US-09-029-755C-1	Sequence 1, App1
C 3	58.3	12665	4	US-08-961-527-134	Sequence 134, App
C 4	58.3	225	4	US-09-134-001C-870	Sequence 870, App
C 5	58.3	834	2	US-08-967-001C-113	Sequence 113, App
C 6	58.3	834	2	US-08-592-541-113	Sequence 113, App
C 7	58.3	834	3	US-09-124-698-113	Sequence 113, App
C 8	58.3	834	4	US-09-127-480-113	Sequence 113, App
C 9	58.3	834	4	US-08-496-841C-113	Sequence 113, App
C 10	58.3	834	4	US-09-124-523-113	Sequence 113, App
C 11	58.3	954	4	US-09-134-001C-875	Sequence 875, App
C 12	58.3	2417	4	US-09-605-785-334	Sequence 334, App
C 13	58.3	2417	4	US-09-439-313-334	Sequence 334, App
C 14	58.3	2417	4	US-09-352-616A-334	Sequence 334, App
C 15	58.3	2417	4	US-09-232-149A-334	Sequence 334, App
C 16	58.3	2560	4	US-08-961-527-114	Sequence 114, App
C 17	58.3	3674	4	US-09-605-785-698	Sequence 698, App
C 18	58.3	56516	2	US-08-996-306-1	Sequence 1, App1
C 19	58.3	56516	4	US-08-338-907-1	Sequence 1, App1
C 20	58.3	56516	4	US-09-218-207-1	Sequence 1, App1
C 21	58.3	56520	4	US-09-338-907-179	Sequence 179, App
C 22	58.3	56520	4	US-09-218-207-179	Sequence 28, App1
C 23	54.2	156	1	US-08-700-575-28	Sequence 28, App1
C 24	54.2	170	3	US-09-035-648-8	Sequence 8, App1
C 25	54.2	170	4	US-09-001-951-8	Sequence 8, App1
C 26	54.2	170	4	US-08-818-829-8	Sequence 8, App1
C 27	54.2	227	4	US-08-991-789A-183	Sequence 183, App

C 28	13	54.2	227	4	US-09-062-451-183	Sequence 183, App
C 29	13	54.2	227	4	US-09-598-326-183	Sequence 183, App
C 30	13	54.2	375	4	US-09-509-902A-13	Sequence 13, App1
C 31	13	54.2	798	1	US-08-133-979A-10	Sequence 10, App1
C 32	13	54.2	798	2	US-08-436-890-10	Sequence 10, App1
C 33	13	54.2	798	2	US-08-451-213-10	Sequence 10, App1
C 34	13	54.2	907	3	US-08-672-850-7	Sequence 7, App1
C 35	13	54.2	907	3	US-08-672-850-11	Sequence 11, App1
C 36	13	54.2	908	4	US-09-457-046B-23	Sequence 23, App1
C 37	13	54.2	1001	3	US-08-672-850-10	Sequence 10, App1
C 38	13	54.2	1001	4	US-09-641-638-405	Sequence 405, App
C 39	13	54.2	1210	2	US-08-483-695-4	Sequence 4, App1
C 40	13	54.2	1210	2	US-07-865-285-4	Sequence 4, App1
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C 42	13	54.2	1210	2	US-09-201-912-4	Sequence 4, App1
C 43	13	54.2	1458	4	US-08-913-578-1	Sequence 1, App1
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C 45	13	54.2	1458	4	US-08-403-634-1	Sequence 1, App1
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C 48	13	54.2	1586	3	US-09-173-581-11	Sequence 11, App1
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C 51	13	54.2	1868	4	US-09-948-802-1	Sequence 1, App1
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C 53	13	54.2	2142	4	US-09-441-039-3	Sequence 3, App1
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C 55	13	54.2	2900	1	US-08-117-362-1	Sequence 1, App1
C 56	13	54.2	2900	1	US-08-486-924-1	Sequence 1, App1
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C 58	13	54.2	4049	1	US-08-162-809-17	Sequence 17, App1
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C 62	13	54.2	246240	2	US-08-724-394A-21	Sequence 21, App1
C 63	13	54.2	246240	2	US-08-724-394A-22	Sequence 22, App1
C 64	12	50.0	62	3	US-09-184-658-65	Sequence 65, App1
C 65	12	50.0	129	4	US-09-219-983A-15	Sequence 15, App1
C 66	12	50.0	367	4	US-09-219-983A-13	Sequence 13, App1
C 67	12	50.0	408	3	US-09-184-658-5	Sequence 5, App1
C 68	12	50.0	573	4	US-09-328-111-221	Sequence 221, App
C 69	12	50.0	658	3	US-08-961-083-27	Sequence 27, App1
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C 72	12	50.0	900	4	US-08-987-121A-1	Sequence 1, App1
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C 75	12	50.0	1006	3	US-08-961-083-51	Sequence 51, App1
C 76	12	50.0	1008	4	US-08-987-121A-5	Sequence 5, App1
C 77	12	50.0	1011	4	US-08-987-121A-3	Sequence 3, App1
C 78	12	50.0	1011	4	US-09-066-512-1	Sequence 1, App1
C 79	12	50.0	1032	4	US-09-227-357-134	Sequence 134, App
C 80	12	50.0	1034	4	US-09-227-357-15	Sequence 15, App1
C 81	12	50.0	1279	1	US-08-146-010A-4	Sequence 4, App1
C 82	12	50.0	1279	1	US-08-674-168-9	Sequence 9, App1
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C 84	12	50.0	1289	2	US-08-761-277A-13	Sequence 13, App1
C 85	12	50.0	1308	1	US-08-691-129-1	Sequence 1, App1
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C 87	12	50.0	1308	1	US-08-818-984-1	Sequence 1, App1
C 88	12	50.0	1308	1	US-08-818-984-3	Sequence 3, App1
C 89	12	50.0	1340	3	US-09-184-658-8	Sequence 8, App1
C 90	12	50.0	1340	2	US-08-672-302-3	Sequence 3, App1
C 91	12	50.0	1410	3	US-08-668-392-1	Sequence 1, App1
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C 95	12	50.0	1456	2	US-08-303-569B-6	Sequence 6, App1
C 96	12	50.0	1570	2	US-08-116-217-35	Sequence 35, App1
C 97	12	50.0	1624	2	US-08-464-517-35	Sequence 35, App1
C 98	12	50.0	1624	2	US-08-246-361A-35	Sequence 35, App1
C 99	12	50.0	1624	3	US-08-463-772-35	Sequence 35, App1
C 100	12	50.0	1624	5	PCT-US93-05000-35	Sequence 35, App1

ALIGNMENTS

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RESULT 1
US-08-858-207A-123/c
; Sequence 123, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Scodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-858-207A-123

Query Match 62.5%; Score 15; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATG 18
Db 296 GTCAAGGCTGTAATG 282

RESULT 2
US-09-029-755C-1/c
; Sequence 1, Application US/09029755C
; Patent No. 6326477
; GENERAL INFORMATION:
; APPLICANT: ILMEN, Maxja
; APPLICANT: SOEDERLUND, Hans
; APPLICANT: PENTTILA, Metja
; TITLE OF INVENTION: PROCESS FOR MODIFYING GLUCOSE REPRESSION
; FILE REFERENCE: Substitute Sequence Listing-09-029755
; Patent No. 6326477
; CURRENT APPLICATION NUMBER: US/09/029,755C

Query Match 62.5%; Score 15; DB 4; Length 12665;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCAAGGCTGTAATG 18
Db 1571 GCTGTAATGATCATC 1557

RESULT 3
US-08-961-527-134
; Sequence 134, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8512
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-134

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Best Local Similarity 100.0%; Pred. No. 1.7;
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Qy 10 GCTGTAATGATCATC 24
Db 1571 GCTGTAATGATCATC 1557
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GenCore version 5.1.3
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and is derived by analysis of the total score distribution.

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5	19	59.4	29	6 AR073461	AR073461 Sequence
6	19	59.4	29	6 AX022055	AX022055 Sequence
7	19	59.4	29	6 I93332	I93332 Sequence 2
8	19	59.4	30	6 AR165158	AR165158 Sequence
9	19	59.4	30	6 I06852	I06852 Sequence 9
10	19	59.4	33	6 AR021438	AR021438 Sequence
11	19	59.4	33	6 AR043000	AR043000 Sequence
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19	19	59.4	42	6 AR161264	AR161264 Sequence
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24	19	59.4	43	6 AR043942	AR043942 Sequence
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26	19	59.4	43	6 AX022069	AX022069 Sequence
27	19	59.4	43	6 I93346	I93346 Sequence 16
28	19	59.4	48	6 I03645	I03645 Sequence 6
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30	19	59.4	98	10 MUSIGRAC2	MUSIGRAC2
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ALIGNMENTS

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LOCUS AR048860 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5824307.
ACCESSION AR048860
VERSION AR048860.1 GI:6004899
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,L.Sid.
TITLE Human-murine chimeric antibodies against respiratory syncytial virus
JOURNAL Patent: US 5824307-A 5 20-OCT-1998;
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BASE COUNT 5 a 5 c 8 g 6 t
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RESULT 2
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LOCUS I32409 24 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 4 from patent US 5587458.
ACCESSION I32409
VERSION I32409.1 GI:1823200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS King,C.Richter., Kasprzyk,P.G. and Bird,R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof
JOURNAL Patent: US 5587458-A 4 24-DEC-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 5 a 5 c 8 g 6 t
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATGATCCAGTTGGTGCGATC 24

RESULT 3
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LOCUS AX060799 20 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 20 from patent WO0078815.
ACCESSION AX060799
VERSION AX060799.1 GI:12406179
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Huse,W.D. and Wu,H.
TITLE Anti-g(a) v?g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
JOURNAL Patent: WO 0078815-A 20 28-DEC-2000;
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/db xref="taxon:32630"
/note="oligonucleotide" 4 t

Query Match 59.4%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CAGTTGGTGCGATCAGC 20

RESULT 4
AR043928
LOCUS AR043928 29 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5817311.
ACCESSION AR043928
VERSION AR043928.1 GI:5965393
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 29)
AUTHORS Bazin,H. and Latinne,D.
TITLE Methods of inhibiting T-cell mediated immune responses with

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 1024 Seconds

(without alignments)
506.109 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

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Post-processing: Listing first 100 summaries

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- 13: gb_est4:*
- 14: gb_est5:*
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- 16: em_estom:*
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- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
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- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	19	59.4	472	10	BE289692 601088922
C 4	19	59.4	489	13	BI110707 602896196
C 5	19	59.4	519	14	BM986669 EST594263
C 6	19	59.4	532	13	BI104783 602891329

C 7	19	59.4	537	14	BQ211527	BQ211527	UI-R-DY1-
C 8	19	59.4	540	10	AW917591	AW917591	EST348935
C 9	19	59.4	540	13	BG964740	BG964740	602829470
C 10	19	59.4	541	13	BM245196	BM245196	K0721C06-
C 11	19	59.4	541	9	AA819712	AA819712	UI-R-A0-a
C 12	19	59.4	553	10	BE309891	BE309891	601091717
C 13	19	59.4	553	13	BM194877	BM194877	L0702E09-
C 14	19	59.4	557	13	BM243211	BM243211	K0645C09-
C 15	19	59.4	559	12	BF580308	BF580308	602097044
C 16	19	59.4	569	13	BG964957	BG964957	602829274
C 17	19	59.4	575	13	BI249452	BI249452	602995789
C 18	19	59.4	577	10	BE305476	BE305476	601099542
C 19	19	59.4	585	13	BM194777	BM194777	L0700H12-
C 20	19	59.4	586	13	BM244148	BM244148	K0707C10-
C 21	19	59.4	594	10	BE309592	BE309592	601094848
C 22	19	59.4	594	14	BQ175706	BQ175706	UI-M-DJ2-
C 23	19	59.4	599	10	BE287315	BE287315	601093986
C 24	19	59.4	606	12	BF139980	BF139980	601791116
C 25	19	59.4	606	14	BQ922747	BQ922747	AGENCOURT
C 26	19	59.4	607	12	BF580281	BF580281	602097014
C 27	19	59.4	611	14	BQ175762	BQ175762	UI-M-DJ2-
C 28	19	59.4	620	10	BE368918	BE368918	601221562
C 29	19	59.4	624	10	BE306691	BE306691	601104076
C 30	19	59.4	626	12	BF582283	BF582283	602101109
C 31	19	59.4	630	12	BF138788	BF138788	601780387
C 32	19	59.4	631	13	BE284233	BE284233	UI-R-DA0-
C 33	19	59.4	638	10	BE284233	BE284233	601099177
C 34	19	59.4	639	12	BF583310	BF583310	602101781
C 35	19	59.4	641	12	BF134573	BF134573	601784982
C 36	19	59.4	643	12	BF579280	BF579280	602093454
C 37	19	59.4	659	12	BF137298	BF137298	601781658
C 38	19	59.4	660	13	BF123478	BF123478	602899340
C 39	19	59.4	669	12	BF123422	BF123422	601760623
C 40	19	59.4	671	13	BM194931	BM194931	L0703D04-
C 41	19	59.4	674	12	BF582339	BF582339	602101170
C 42	19	59.4	678	13	BG962941	BG962941	602827925
C 43	19	59.4	680	10	BE376043	BE376043	601229480
C 44	19	59.4	683	12	BF582936	BF582936	602101386
C 45	19	59.4	683	13	BI279213	BI279213	UI-R-DA0-
C 46	19	59.4	685	10	BE369854	BE369854	601212655
C 47	19	59.4	685	12	BG518843	BG518843	602578277
C 48	19	59.4	691	10	BE307937	BE307937	601096061
C 49	19	59.4	691	13	BI274417	BI274417	UI-R-CW0-
C 50	19	59.4	692	14	BQ198766	BQ198766	UI-R-EB0-
C 51	19	59.4	693	13	BG964281	BG964281	602833907
C 52	19	59.4	693	13	BM171763	BM171763	imageGCG.5
C 53	19	59.4	694	13	BG971707	BG971707	602838232
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C 56	19	59.4	704	12	BF580765	BF580765	602093921
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C 60	19	59.4	707	13	BI250555	BI250555	602993614
C 61	19	59.4	708	10	BE309445	BE309445	601095331
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C 66	19	59.4	713	13	BI113389	BI113389	602900996
C 67	19	59.4	714	13	BG963548	BG963548	602831226
C 68	19	59.4	716	13	BG964192	BG964192	602828968
C 69	19	59.4	721	13	BG967689	BG967689	602833496
C 70	19	59.4	722	12	BF140170	BF140170	601786735
C 71	19	59.4	725	12	BF580940	BF580940	602100636
C 72	19	59.4	725	13	BG963055	BG963055	602828068
C 73	19	59.4	728	13	BG962985	BG962985	602827980
C 74	19	59.4	728	14	BQ139055	BQ139055	UI-R-EB0-
C 75	19	59.4	732	13	BG962768	BG962768	602830291
C 76	19	59.4	732	13	BG967206	BG967206	602099743
C 77	19	59.4	738	12	BF582153	BF582153	602099743
C 78	19	59.4	743	13	BG968770	BG968770	602836677
C 79	19	59.4	743	13	BI106381	BI106381	602892928

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C 80      19 59.4 748 13 BG963884 602828572
C 81      19 59.4 750 13 BG965050
C 82      19 59.4 751 13 BG966164 602830119
C 83      19 59.4 753 13 BG966417 602832922
C 84      19 59.4 754 13 BG967635 602833433
C 85      19 59.4 754 14 BQ198977 UI-R-PAO-
C 86      19 59.4 755 13 BQ198977 602833433
C 87      19 59.4 755 13 B1150509 6028915167
C 88      19 59.4 762 12 BF144806 601791486
C 89      19 59.4 764 13 B1455283 603171949
C 90      19 59.4 766 13 BG967034 602834270
C 91      19 59.4 770 13 BG965872 602829638
C 92      19 59.4 772 10 BE285427 601096728
C 93      19 59.4 772 12 BF581992 602099448
C 94      19 59.4 772 13 B1105452 602891971
C 95      19 59.4 774 12 BF581989 602099444
C 96      19 59.4 774 12 BF123744 601760491
C 97      19 59.4 778 13 BG964076 602828830
C 98      19 59.4 781 13 B1152656 602918350
C 99      19 59.4 785 14 BQ940341 AGENCOURT
C 100     19 59.4 793 10 BE307894 601096548

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ALIGNMENTS

```

RESULT 1
BF139390/c
LOCUS      BF139390      1063 bp      mRNA      linear      EST 24-OCT-2000
DEFINITION 601785258F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4013126 5',
            mRNA sequence.
ACCESSION  BF139390
VERSION     BF139390.1 GI:10978430
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 1063)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: c9apbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9255 row: c column: 15
            High quality sequence stop: 635.
            Location/Qualifiers
                1..1063
                /organism="Mus musculus"
                /strain="CZECH II"
                /db_xref="taxon:10090"
                /clone="IMAGE:4013126"
                /clone_lib="NCI_CGAP_Lu30"
                /tissue_type="tumor, metastatic to mammary"
                /lab_host="DH10B"
                /note="Organ: lung; Vector: pCMV-SPORT6; Site:1: NotI;
                Site 2: SalI; transgenic model WNT-1, expression driven by
                MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
                dT. Library constructed by Life Technologies.
                Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      297 a      277 c      238 g      251 t
ORIGIN

```

FEATURES

```

source
Query Match      62.5%; Score 20; DB 12; Length 1063;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match      59.4%; Score 19; DB 14; Length 464;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match      62.5%; Score 20; DB 12; Length 1063;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      13  CCAGTTGGTGCGAGCATCAGC 32
          |||||
DB      421  CCAGTTGGTGCGAGCATCAGC 402
          |||||

RESULT 2
BM986668      464 bp      mRNA      linear      EST 25-MAR-2002
LOCUS      BM986668      464 bp      mRNA      linear      EST 25-MAR-2002
DEFINITION  EST594262 Rat gene index, normalized rat, norvegicus Rattus
            norvegicus cDNA clone RGOAD95 3' end similar to anti-acetylcholine
            receptor antibody, mRNA sequence.
ACCESSION  BM986668
VERSION     BM986668
KEYWORDS   EST.
SOURCE     BM986668.1 GI:19706057
            Norway rat.
            Rattus norvegicus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 464)
            Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G.,
            Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.
            Generation of ESTs from a rat multiple tissue survey
            Unpublished (2001)
            Other ESTs: EST594263
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            This clone is available through the ATCC, contact the ATCC
            tel#703-365-2700 for further information
            Seq primer: M13 forward.

```

FEATURES

```

source
1..464
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGOAD95"
/clone_lib="Rat gene index, normalized rat, norvegicus"
/tissue_type="mixed tissue"
/note="Vector: p773pac; Site 1: EcoRI; Site 2: NotI;
Combination of untreated and NGF-treated PC12 cell
libraries, and Bento Soares normalized libraries of ovary,
brain, kidney, liver, placenta, lung, embryo, skeletal
muscle, spleen, heart"
BASE COUNT      102 a      112 c      121 g      129 t
ORIGIN
Query Match      59.4%; Score 19; DB 14; Length 464;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14  CAGTTGGTGCGAGCATCAGC 32
          |||||
DB      334  CAGTTGGTGCGAGCATCAGC 352
          |||||

RESULT 3
BE289692/c
LOCUS      BE289692      472 bp      mRNA      linear      EST 26-OCT-2000
DEFINITION  601088922F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3483797 5',
            mRNA sequence.
ACCESSION  BE289692
VERSION     BE289692.1 GI:9170234
KEYWORDS   EST.
SOURCE     house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 472)
            NIH-MGC http://mgc.nci.nih.gov/.

```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 128.976 Seconds

(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

Sequence: 1 gggaagatgcatccagttgtgcagcatcagc 32

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wc size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_101002.*

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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	75.0	24	AA116189	Anti-RSV F protein
2	75.0	24	AA165009	Anti-EBV2 antibody
3	59.4	20	AAV49835	LM609 grafted anti
4	59.4	20	AAV84782	HC and K antibody
5	59.4	20	AAH74638	PCR primer for lig
6	59.4	20	AA28190	Primer #2. Uniden
7	59.4	24	AA062720	Probe for detectio
8	59.4	24	AA062721	Probe for detectio
9	59.4	28	AAV45322	Kappa back primer.

10	19	59.4	28	AAV45318	FvK back primer.
11	19	59.4	29	AA071880	Lo-CD2a CL antisen
12	19	59.4	29	AAV62598	Lo-CD2a chimeric a
13	19	59.4	29	AAV22856	Lo-CD2a light chai
14	19	59.4	29	AAZ10123	Primer CL antisens
15	19	59.4	30	AAV35273	PCR primer used to
16	19	59.4	30	AAZ26147	PCR primer C-kappa
17	19	59.4	32	AAZ28085	Fusion gene huKS-m
18	19	59.4	32	AAZ31014	PCR primer used to
19	19	59.4	32	AAZ31545	PCR primer C-mu us
20	19	59.4	32	ABA99123	Sense primer #1 us
21	19	59.4	33	AAQ4196	PCR primer to ampl
22	19	59.4	33	AAAT37284	Mouse IgM light ch
23	19	59.4	33	AAV12579	Primer for mouse I
24	19	59.4	33	AAV73482	Mouse Igkappa cons
25	19	59.4	33	AAV38177	PCR primer for mou
26	19	59.4	33	AAZ21967	PCR primer used to
27	19	59.4	38	AAO53439	Sequence reverse C
28	19	59.4	39	AAV05548	S19 Mb kappa ligh
29	19	59.4	40	AAV09305	Murine anti-Protei
30	19	59.4	41	AAQ4387	Kappa II primer.
31	19	59.4	42	AAQ23440	Kappa light chain
32	19	59.4	42	AAQ44174	C-kappa light chai
33	19	59.4	42	AAQ4174	Probe specific for
34	19	59.4	42	AAV12529	Probe for mouse ka
35	19	59.4	42	AAV70512	Mouse Immunoglobul
36	19	59.4	42	AAV73463	Mouse kappa chain
37	19	59.4	42	AAV38146	Probe for the mous
38	19	59.4	42	AAZ21885	Probe used to isol
39	19	59.4	42	AAV06028	Mouse light chain
40	19	59.4	42	ABK43218	Recombinant adenov
41	19	59.4	43	AAQ71893	Lo-CD2a VK PCR pri
42	19	59.4	43	AAV62612	Lo-CD2a chimeric a
43	19	59.4	43	AAV22868	Lo-CD2a primer 3'
44	19	59.4	43	AAZ10137	PCR primer used to
45	19	59.4	44	AAQ78721	Primer to amplify
46	19	59.4	45	AAQ78720	Primer to amplify
47	19	59.4	145	AAZ22762	Partial scFv1F1-GF
48	19	59.4	318	AAZ28960	Mouse antibody 1C3
49	19	59.4	42	AAH27466	Murine coding sequ
50	19	59.4	349	AAV19521	Monoclonal antibod
51	19	59.4	354	AAI65596	Phosphonate ester
52	19	59.4	357	AAV1270	Anti-CEA antibody
53	19	59.4	358	AAQ5683	Sequence encoding
54	19	59.4	360	AAQ90434	DNA encoding anti-
55	19	59.4	360	AAV96344	cDNA for Ig light
56	19	59.4	360	AAZ39342	Rat anti-interleuk
57	19	59.4	363	AAQ37472	Sequence encoding
58	19	59.4	363	AAQ53992	LS2H241 light chai
59	19	59.4	363	AAQ56686	Sequence of the mo
60	19	59.4	363	AAQ56688	Sequence of the mo
61	19	59.4	363	AAV38510	Light chain coding
62	19	59.4	363	AAV47893	Monoclonal antibod
63	19	59.4	363	AAV47895	MbD-N01 light ch
64	19	59.4	363	AAV13951	Mouse J591 monoclo
65	19	59.4	363	AAV37832	J591 monoclonal an
66	19	59.4	363	AAQ65542	Murine monoclonal
67	19	59.4	364	AAV34816	Humanised anti-CD3
68	19	59.4	365	AAH41750	Monoclonal antibod
69	19	59.4	366	AAQ27140	ICM-1 inhibiting
70	19	59.4	368	AAV05543	Nucleotide sequenc
71	19	59.4	368	AAV09793	DNA encoding the l
72	19	59.4	387	ABL53530	Anti-RANK ligand m
73	19	59.4	388	AAV66674	Anti-Fas MAb CH11
74	19	59.4	388	AAV78206	Anti-human Fas ant
75	19	59.4	391	AAV03378	Anti-IL-8 MAb 6G4.
76	19	59.4	391	AAV03224	Anti-IL-8 antibody
77	19	59.4	391	AAV93547	Murine MAb (6G4.2.
78	19	59.4	391	AAV78588	Monoclonal antibod
79	19	59.4	391	AAV44949	Murine anti-IL-8 M
80	19	59.4	391	AAV10310	Murine monoclonal
81	19	59.4	391	AAV06415	Murine MAb (6G4.2.
82	19	59.4	391	AAV90571	Murine 6G4.2.5 mon

C 83 19 59.4 391 21 AAC65499 Murine 6G4-2-5 ant
 C 84 19 59.4 391 21 AAZ87960 Humanised 6G4-2.5
 C 85 19 59.4 396 22 AAH41752 Monoclonal antibod
 C 86 19 59.4 404 22 AAF81911 Anti-CA125 bifunct
 C 87 19 59.4 407 13 AAQ28254 VL FRP5. Mus musc
 C 88 19 59.4 407 21 AAZ49548 Mouse light chain
 C 89 19 59.4 418 17 AAT34152 Monoclonal antibod
 C 90 19 59.4 420 10 AAN90672 DNA sequence encod
 C 91 19 59.4 420 10 AAV60831 Variable light cha
 C 92 19 59.4 426 16 AAQ99848 Rat monoclonal ant
 C 93 19 59.4 426 22 AAD13177 Murine antibody ID
 C 94 19 59.4 429 18 AAT70811 Mouse anti-idiotyp
 C 95 19 59.4 432 12 AAQ15114 IL-2 chimeric anti
 C 96 19 59.4 435 12 AAQ15115 IL-2 chimeric anti
 C 97 19 59.4 435 14 AAQ36613 Anti-IL2R-alpha an
 C 98 19 59.4 435 18 AAT85149 Murine monoclonal
 C 99 19 59.4 435 20 AAV83772 Antibody 11D10 lig
 C 100 19 59.4 438 16 AAQ90431 DNA encoding anti-

ALIGNMENTS

RESULT 1

AAT16189
 ID AAT16189 standard; DNA; 24 BP.

AC AAT16189;
 DT 16-MAY-1996 (first entry)
 XX
 DE Anti-RSV F protein MAB 1129 VL PCR primer SJ11.
 XX
 KW Humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB 1129; respiratory syncytial virus; RSV;
 KW light chain; complementarity determining region; CDR; primer; PCR;
 KW polymerase chain reaction; ss.

OS Synthetic.

XX WO9605229-A1.
 PN

XX 22-FEB-1996.
 PD

XX 09-AUG-1995; 95WO-US10053.
 PF

XX 15-AUG-1994; 94US-0290592.
 PR

XX (MEDI-) MEDIMMUNE INC.
 PA

XX Johnson LS;
 PI

XX WPI; 1996-139646/14.
 DR

XX New chimeric antibodies against respiratory syncytial virus -
 PT comprise human antibodies with CDR's from the variable heavy and
 PT light chains of a murine antibody
 PT

XX Example 7; Page 18; 55pp; English.
 PS

XX Primers SJ42 (AAT16191) and SJ10 (AAT16188) were used to amplify
 CC cDNA from the murine monoclonal antibody (MAB) 1129 VH region.
 CC Primers SJ41 (AAT16190) and SJ11 (AAT16189) were similarly used to
 CC amplify the MAB 1129 VL region. MAB 1129 is active against
 CC respiratory syncytial virus (RSV) glycoprotein F antigenic site
 CC C. Mouse-human chimeric antibodies useful for treatment of RSV
 CC infection have been produced utilising the complementarity
 CC determining regions of the MAB 1129 VL and VH.
 CC

SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;

Query Match 75.0%; Score 24; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 GATGATCCAGTTGGTGCAGCATC 29
 Db 1 GATGATCCAGTTGGTGCAGCATC 24

RESULT 2

AAT65009
 ID AAT65009 standard; DNA; 24 BP.

XX AAT65009;
 AC

XX 05-JUN-1997 (first entry)
 DT

XX Anti-erbB2 antibody e23 light chain PCR primer.
 DE

XX Single chain antibody; variable region; light chain; heavy chain;
 KW breast cancer; ovarian cancer; non-small cell lung carcinoma;
 KW immunodiagnosis; treatment; cytotoxic agent; erbB-2; ss.

XX Synthetic.
 OS

XX US5587458-A.
 FN

XX 24-DEC-1996.
 PD

XX 07-OCT-1991; 91US-0772270.
 PF

XX 14-MAY-1993; 93US-0061092.
 PR

XX 07-OCT-1991; 91US-0772270.
 PR

XX 30-JUN-1992; 92US-0906555.
 PR

XX (ARON-) ARONEX PHARM INC.
 PA

XX Bird RE, Kasprzyk PG, King CR;
 PI

XX WPI; 1997-064831/06.
 DR

XX Single chain antibodies specific for erbB-2 protein, gp185 - with
 PT labels or cytotoxin, useful for detection and treatment of tumour
 PT cells expressing this protein
 PT

XX Example 8; Column 18; 28pp; English.
 PS

XX Monoclonal antibody e23 was generated by immunising mice with
 CC N/erbB-2 cells overexpressing the gp185 protein, removing spleen
 CC cells and producing hybridomas by standard techniques. Messenger
 CC RNA coding for the anti-erbB-2 monoclonal antibody was isolated
 CC and converted to cDNA. Regions coding for the heavy- and light-
 CC chain variable regions were then amplified by PCR using primers
 CC having the sequences given in AAT65008-T65011 and joined via a
 CC sequence encoding a peptide linker. The resulting single-chain
 CC antibody, designated e23(Fv), is useful for in vitro diagnosis of
 CC tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast,
 CC ovarian and non-small cell lung carcinomas, and, when coupled to a
 CC cytotoxic agent, to treat such tumours.
 CC

SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;

Query Match 75.0%; Score 24; DB 18; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GATGATCCAGTTGGTGCAGCATC 29
 Db 1 GATGATCCAGTTGGTGCAGCATC 24

RESULT 3

AAV49835
 ID AAV49835 standard; DNA; 20 BP.

XX

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 24.9756 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Wsize : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	19	59.4	358	US-09-800-908-10	Sequence 10, Appli
7	19	59.4	360	US-09-905-243-65	Sequence 65, Appli
8	19	59.4	363	US-09-929-665-9	Sequence 9, Appli
9	19	59.4	363	US-09-929-665-10	Sequence 10, Appli
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C 23	19	59.4	504	12	US-10-006-773-14	Sequence 14, Appli
C 24	19	59.4	698	12	US-10-006-773-18	Sequence 18, Appli
C 25	19	59.4	729	12	US-10-006-773-10	Sequence 10, Appli
C 26	19	59.4	809	12	US-10-027-770-1	Sequence 1, Appli
C 27	19	59.4	831	9	US-09-903-327A-3	Sequence 3, Appli
C 28	19	59.4	1085	10	US-09-815-837-81	Sequence 81, Appli
C 29	19	59.4	1159	10	US-09-917-800A-1410	Sequence 1410, Ap
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C 32	19	59.4	1161	10	US-09-917-800A-1411	Sequence 1411, Ap
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C 35	19	59.4	1686	10	US-09-815-837-65	Sequence 65, Appli
C 36	19	59.4	1698	10	US-09-815-837-79	Sequence 79, Appli
C 37	19	59.4	5691	10	US-09-897-006-11	Sequence 11, Appli
C 38	19	59.4	5711	10	US-09-897-006-8	Sequence 8, Appli
C 39	19	59.4	6255	10	US-09-897-006-13	Sequence 13, Appli
C 40	18	56.2	293	10	US-09-867-701-5755	Sequence 5755, Ap
C 41	18	56.2	939	10	US-09-867-550-1621	Sequence 1621, Ap
C 42	16	50.0	30	10	US-09-855-221-4	Sequence 4, Appli
C 43	16	50.0	30	10	US-09-949-559-52	Sequence 52, Appli
C 44	16	50.0	38	9	US-09-991-470-19	Sequence 19, Appli
C 45	16	50.0	40	10	US-09-874-547-34	Sequence 34, Appli
C 46	16	50.0	354	10	US-09-949-559-105	Sequence 105, App
C 47	16	50.0	363	10	US-09-965-099-5	Sequence 5, Appli
C 48	16	50.0	363	12	US-10-051-852-5	Sequence 5, Appli
C 49	16	50.0	407	10	US-09-983-965-4802	Sequence 4802, Ap
C 50	15	46.9	39	10	US-09-859-214-63	Sequence 63, Appli
C 51	15	46.9	481	10	US-09-881-823-13	Sequence 13, Appli
C 52	15	46.9	1222	10	US-09-754-016-3	Sequence 3, Appli
C 53	15	46.9	1578	10	US-09-804-551B-35	Sequence 35, Appli
C 54	15	46.9	1934	10	US-09-754-016-1	Sequence 1, Appli
C 55	15	46.9	2519	10	US-09-917-800A-1647	Sequence 1647, Ap
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C 59	14	43.8	252	10	US-09-923-876-1845	Sequence 1845, Ap
C 60	14	43.8	309	10	US-09-954-456-196	Sequence 196, App
C 61	14	43.8	349	9	US-09-796-692-2634	Sequence 2634, Ap
C 62	14	43.8	370	10	US-09-880-107-804	Sequence 804, App
C 63	14	43.8	402	10	US-09-974-300-154	Sequence 154, App
C 64	14	43.8	460	9	US-10-046-935-73	Sequence 73, Appli
C 65	14	43.8	460	9	US-09-878-178-73	Sequence 73, Appli
C 66	14	43.8	637	10	US-09-770-119-635	Sequence 635, App
C 67	14	43.8	678	10	US-09-867-550-1347	Sequence 1347, Ap
C 68	14	43.8	770	10	US-09-910-943-27	Sequence 27, Appli
C 69	14	43.8	1110	9	US-10-041-006A-1	Sequence 1, Appli
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C 71	14	43.8	1129	9	US-10-028-072-221	Sequence 221, App
C 72	14	43.8	1130	9	US-10-041-006A-8	Sequence 8, Appli
C 73	14	43.8	1130	12	US-10-040-655-8	Sequence 8, Appli
C 74	14	43.8	1146	10	US-09-764-855-205	Sequence 205, App
C 75	14	43.8	1241	8	US-08-881-509-1	Sequence 1, Appli
C 76	14	43.8	1386	10	US-09-823-830A-384	Sequence 384, App
C 77	14	43.8	1454	12	US-10-002-600-101	Sequence 101, App
C 78	14	43.8	1547	9	US-09-978-295A-465	Sequence 465, App
C 79	14	43.8	1547	9	US-09-978-697-465	Sequence 465, App
C 80	14	43.8	1547	9	US-09-978-192A-465	Sequence 465, App
C 81	14	43.8	1547	9	US-09-999-832A-465	Sequence 465, App
C 82	14	43.8	1547	9	US-09-978-189-465	Sequence 465, App
C 83	14	43.8	1547	9	US-10-028-072-417	Sequence 417, App
C 84	14	43.8	1552	9	US-09-764-841-21	Sequence 21, Appli
C 85	14	43.8	1561	9	US-10-098-841-24	Sequence 24, Appli
C 86	14	43.8	1637	9	US-09-738-628-3076	Sequence 3076, Ap
C 87	14	43.8	1854	9	US-09-822-849A-267	Sequence 267, App
C 88	14	43.8	1941	10	US-09-822-849A-267	Sequence 267, App
C 89	14	43.8	2084	10	US-09-764-851-13	Sequence 13, Appli
C 90	14	43.8	2233	9	US-09-350-874-54	Sequence 54, Appli
C 91	14	43.8	4148	10	US-10-098-841-205	Sequence 205, App
C 92	14	43.8	4253	9	US-10-098-841-205	Sequence 205, App

Sequence 1790, Ap
Sequence 1791, Ap
Sequence 2811, Ap
Sequence 2812, Ap
Sequence 7, Appl1
Sequence 302, App
Sequence 527, App
Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-09-158-120A-5
; Sequence 5, Application US/09158120A
; Patent No. US20020102257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: P160
OPERATING SYSTEM: Windows95
SOFTWARE: MS Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158.120A
FILING DATE: September 21, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290.592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813.372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide

US-09-158-120A-5
Query Match 75.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GATGGATCCAGTTGGTGCGAGCATC 29
Db 1 GATGGATCCAGTTGGTGCGAGCATC 24

RESULT 2
US-08-790-540A-20
; Sequence 20, Application US/08790540A
; Patent No. US2001001125A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

US-08-791-391A-20
Query Match 59.4%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAGTTGGTGCGAGCATCAGC 32
Db 2 CAGTTGGTGCGAGCATCAGC 20

RESULT 3
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; Sequence 20, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
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; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/790,540A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-790-540A-20

Query Match 59.4%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAGTTGGTGCGAGCATCAGC 32
Db 2 CAGTTGGTGCGAGCATCAGC 20

RESULT 3
US-08-791-391A-20
; Sequence 20, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

US-08-791-391A-20
Query Match 59.4%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAGTTGGTGCGAGCATCAGC 32
Db 2 CAGTTGGTGCGAGCATCAGC 20

RESULT 3
US-08-791-391A-20
; Sequence 20, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
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; STATE: California
; COUNTRY: United States
; ZIP: 92122
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

US-08-791-391A-20
Query Match 59.4%; Score 19; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CAGTTGGTGCGAGCATCAGC 32
Db 2 CAGTTGGTGCGAGCATCAGC 20

RESULT 3
US-08-791-391A-20
; Sequence 20, Application US/08791391A
; Patent No. US20010016645A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
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; CORRESPONDENCE ADDRESS:
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; STATE: California
; COUNTRY: United States
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,391A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 25.561 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-8

Perfect score: 32

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	24	75.0	24	5 PCT-US96-09448-5	Sequence 5, Appli
5	19	59.4	20	3 US-08-832-985-83	Sequence 83, Appli
6	19	59.4	20	4 US-09-410-903-64	Sequence 64, Appli
7	19	59.4	29	1 US-08-477-877B-2	Sequence 2, Appli
8	19	59.4	29	1 US-08-472-81A-2	Sequence 2, Appli
9	19	59.4	29	2 US-08-477-989B-2	Sequence 2, Appli
10	19	59.4	30	3 US-08-582-740-3	Sequence 3, Appli
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20	19	59.4	39	2 US-08-671-622-6	Sequence 6, Appli
21	19	59.4	40	5 PCT-US95-07372-4	Sequence 4, Appli
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; Sequence 4, Application US/08061092A
; Patent No. 5587458
; GENERAL INFORMATION:
; APPLICANT: KING, C R
; APPLICANT: KASPRZYK, Philip G
; APPLICANT: BIRD, Robert E
; TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS
; TITLE OF INVENTION: THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061,092A
; FILING DATE: 14-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 018797-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-061-092A-4

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
; ADDRESSEE: OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

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ALIGNMENTS

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artificial sequences.
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AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
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Illumina, Inc. (US)
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VERSION AX446316.1 GI:21695215
KEYWORDS
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ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 2771 28-FEB-2002;
Illumina, Inc. (US)
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VERSION AX203833.1 GI:15393278
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artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schall,T.J., Talbot,D., Miao,Z. and Wei,Z.
TITLE Tethered ligands and methods of use
JOURNAL Patent: WO 0146698-A 92 28-JUN-2001;
Chemocentryx, Inc. (US)
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ACCESSION AX203835
VERSION AX203835.1 GI:15393280
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artificial sequences.
REFERENCE 1 (bases 1 to 31)
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AF131192 Mus muscu
AF131193 Mus muscu
US5616 Mus musculu
US5663 Mus musculu
X59088 M.musculus
AF159919 Euplotes
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GenCore version 5.1.3
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82 11 34.4 165 9 AV059436
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84 11 34.4 165 12 B0624408
85 11 34.4 165 14 BQ310451
86 11 34.4 166 9 AI572747
87 11 34.4 166 14 BQ327161
88 11 34.4 167 9 AA284173
89 11 34.4 168 12 BF854470
90 11 34.4 168 14 BQ342862
91 11 34.4 169 9 AV060158
92 11 34.4 169 12 BF920277
93 11 34.4 169 14 D43538
94 11 34.4 171 12 BF823572
95 11 34.4 171 12 BF846944
96 11 34.4 171 14 BQ505576
97 11 34.4 172 9 AV142058
98 11 34.4 174 10 AW597658
99 11 34.4 174 12 BF287879
100 11 34.4 174 13 BI192240

```

ALIGNMENTS

```

RESULT 1
H93873
LOCUS
DEFINITION
H93873.1 Soares fetal liver spleen INFLS Homo sapiens EST 04-DEC-1995
IMAGE: 242146 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR
(HUMAN); mRNA sequence.
H93873
H93873.1 GI:1101169
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 41)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Woldman, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: M13RP1.

```

FEATURES

```

source
1..41
/organism="Homo sapiens"
/db_xref="GDB:3791279"
/db_xref="taxon:9606"
/clone="IMAGE:242146"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGATTAATTAAGACTTTTITTTTTTTTTTTT 3'],"

```

```

double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 7 a 15 c 10 t
ORIGIN

```

```

Query Match 34.4%; Score 11; DB 14; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 TCTCCAGCAAT 32
|||||
DB 26 TCTCCAGCAAT 36
|||||

```

```

RESULT 2
BH789692
LOCUS
DEFINITION
BH789692 51 bp DNA linear GSS 02-APR-20
Arabidopsis thaliana genomic clone SALK_044478.47.05.x, DNA
sequence.
ACCESSION
BH789692
VERSION
BH789692.1 GI:19882790
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 51)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab,
C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At1g01330.
Class: TDNA tagged.

```

FEATURES

```

source
1..51
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_044478.47.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 12 a 7 c 9 g 23 t
ORIGIN

```

```

Query Match 34.4%; Score 11; DB 17; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGATATCGT 11
|||||
DB 35 GGTGATATCGT 45
|||||

```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 128.976 Seconds
(without alignments)
558.741 Million cell updates/sec

Title: US-09-424-705B-9

Perfect score: 32
Sequence: 1 ggtgatcgtctccacacacatccacgaat 32

Scoring table: OLIGO NUC
Gapox 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Mask size: 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: N_Geneseq_101002.*

1: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	32	21	AAA15021
2	23	71.9	33	21	AAK99179
3	23	71.9	33	21	ABK15810
4	11	34.4	24	22	ABO06712
5	11	34.4	24	24	ABO02764
6	11	34.4	24	24	ABO09419
7	11	34.4	24	24	ABO09460
8	11	34.4	30	21	AAA64461
9	11	34.4	40	21	AAZ43423

10	11	34.4	42	21	AAA50168	Antibody 5H7 light
11	11	34.4	47	13	AAQ27347	HindIII-SacI frag
12	11	34.4	47	22	AAK086569	Primer used to amp
13	11	34.4	50	22	AAK086573	Primer used to amp
14	11	34.4	60	24	ABN39364	Human spliced tran
15	11	34.4	65	24	ABN28639	Rat spliced trans
16	11	34.4	65	24	ABN53576	Mouse spliced tran
17	11	34.4	69	20	AAK05584	Anti-Staph (HAY) 9
18	11	34.4	71	24	AAD28222	TOP2 RNA used for
19	11	34.4	73	24	ABK09629	Human ovarian tumo
20	11	34.4	74	24	AAD28302	Alternative versio
21	11	34.4	97	22	ABK73158	Human foetal liver
22	11	34.4	97	22	AAK21593	Human brain expres
23	11	34.4	97	22	AAK47154	Human bone marrow
24	11	34.4	97	22	AAI53587	Probe #22273 used
25	11	34.4	109	24	ABL81083	Human ovarian can
26	11	34.4	118	22	ABK70641	Human foetal liver
27	11	34.4	118	22	ABK37201	Probe #15667 for g
28	11	34.4	118	22	AAK18887	Human brain expres
29	11	34.4	118	22	AAK44831	Human bone marrow
30	11	34.4	118	22	AAI25037	Probe #14970 for g
31	11	34.4	118	22	AAI50808	Probe #19494 used
32	11	34.4	118	24	ABK19070	Human genome-deriv
33	11	34.4	121	22	ABK78171	BRCA1 mutation cor
34	11	34.4	121	22	ABK78172	BRCA1 mutation cor
35	11	34.4	121	22	ABK78175	BRCA1 mutation cor
36	11	34.4	121	22	ABK78176	BRCA1 mutation cor
37	11	34.4	121	22	ABK78179	BRCA1 mutation cor
38	11	34.4	121	22	ABK78180	BRCA1 mutation cor
39	11	34.4	141	18	AAV75623	Staphylococcus aur
40	11	34.4	153	23	ABK27987	Drosophila melanog
41	11	34.4	153	23	AAK49766	Staphylococcus aur
42	11	34.4	153	23	AAK49789	Staphylococcus aur
43	11	34.4	153	23	AAK49910	Staphylococcus aur
44	11	34.4	153	23	AAK50727	Staphylococcus aur
45	11	34.4	167	21	AAK11825	Aspergillus niger
46	11	34.4	169	23	AAK50537	Staphylococcus aur
47	11	34.4	171	23	AAK50214	Staphylococcus aur
48	11	34.4	186	24	ABK76072	Corn tassal-derive
49	11	34.4	208	18	AAV75403	Staphylococcus aur
50	11	34.4	222	22	AAK114181	Human breast cance
51	11	34.4	228	24	ABK67749	Listeria innocua D
52	11	34.4	228	24	ABK69570	Listeria innocua D
53	11	34.4	238	22	AAK78764	Pepermint plant c
54	11	34.4	240	23	AAK48929	Staphylococcus aur
55	11	34.4	240	23	AAK48972	Staphylococcus aur
56	11	34.4	246	24	ABK17374	Human OREF polynuc
57	11	34.4	254	24	ABN27041	Human OREF polynuc
58	11	34.4	271	18	AAV77397	Staphylococcus aur
59	11	34.4	273	21	AAK06547	Human secreted pro
60	11	34.4	274	18	AAV78772	Staphylococcus aur
61	11	34.4	275	22	AAK23043	Human breast cance
62	11	34.4	276	24	ABK70942	Corn tassal-derive
63	11	34.4	277	16	AAK26692	Human gene signatu
64	11	34.4	280	24	ABK16705	Human OREF polynuc
65	11	34.4	281	22	ABK48302	Human breast cell
66	11	34.4	281	22	ABK66187	Human foetal liver
67	11	34.4	281	22	ABK33254	Probe #11720 for g
68	11	34.4	281	22	AAK14606	Human brain expres
69	11	34.4	281	22	AAK40350	Human bone marrow
70	11	34.4	281	22	AAI21107	Probe #11040 for g
71	11	34.4	281	22	AAI46372	Probe #15058 used
72	11	34.4	281	22	AAI06828	Probe #6819 used t
73	11	34.4	281	24	ABK14367	Human genome-deriv
74	11	34.4	296	24	ABK77887	Human OREF polynuc
75	11	34.4	296	24	ABN27242	Human secreted pro
76	11	34.4	298	21	AAK06215	Human genome-deriv
77	11	34.4	300	11	AAK06215	Monoclonal antibod
78	11	34.4	300	17	AAK63504	Monoclonal antibod
79	11	34.4	300	17	AAK63504	Monoclonal antibod
80	11	34.4	300	20	AAK12599	Human gene express
81	11	34.4	300	20	AAK12599	Human gene express
82	11	34.4	300	20	AAK12599	Human gene express

83 11 34.4 300 21 AAC03010 Human secreted pro
 84 11 34.4 302 20 AAX51691 Human secreted pro
 85 11 34.4 306 11 AAQ06228 VK domain of antib
 86 11 34.4 306 17 AAT63506 Monoclonal antibod
 87 11 34.4 306 17 AAT36660 Monoclonal antibod
 88 11 34.4 307 24 ABN20031 Human ORFX polynuc
 89 11 34.4 309 14 AAQ45948 MAb BW 2128 light
 90 11 34.4 315 22 AAL12887 Human breast cance
 91 11 34.4 315 22 AAL21758 Human breast cance
 92 11 34.4 315 24 ABN16562 Human ORFX polynuc
 93 11 34.4 316 21 AAC02853 Human secreted pro
 94 11 34.4 318 14 AAQ36942 VK fragment of ant
 95 11 34.4 318 17 AAT13271 Mucin-type synthe
 96 11 34.4 318 18 AAT79900 Anti-Factor IX MAb
 97 11 34.4 318 22 AAD21670 Humanised antibody
 98 11 34.4 318 22 AAF88095 H. pylori catalase
 99 11 34.4 318 22 AAF88152 H. pylori catalase
 100 11 34.4 318 24 ABK24005 Mouse-human light

ALIGNMENTS

RESULT 1
 AAA15021
 ID AAA15021 standard; DNA; 32 BP.
 CC
 XX AAA15021;
 DT
 XX 21-AUG-2000 (first entry)
 DE PCR primer used to amplify DNA encoding a murine kappa light chain.
 KW CD20-specific receptor; CD-20 specific redirected T cell; leukemia;
 KW CD20+ malignancy; non-Hodgkin's lymphoma; myeloablative chemotherapy;
 KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis;
 KW PCR primer; ss.
 XX Mus sp.
 OS
 XX WO200023573-A2.
 PN
 XX 27-APR-2000.
 PD
 XX 20-OCT-1999; 9SWO-US24484.
 PF
 XX 20-OCT-1998; 98US-0105014.
 PR
 XX (CITY) CITY OF HOPE.
 PA
 XX Raubitschek A, Jensen MC, Wu AM;
 PI
 XX WPI; 2000-339676/29.
 DR
 XX Genetically engineered CD20-specific redirected T cells useful for
 PT treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+
 PT acute or chronic leukemia, and autoimmune disease .
 XX
 PS Example 1; Page 56; 58pp; English.
 CC PCR primers AAA15020-21 were used to amplify DNA encoding a murine
 CC kappa light chain. The amplified sequence was used to construct a
 CC synthetic CD20-specific chimeric receptor. The specification describes
 CC CD-20 specific redirected T cells which express and bear on the cell
 CC surface membrane a CD20-chimeric receptor comprising an intracellular
 CC signalling domain, a transmembrane domain and an extracellular domain,
 CC the extracellular domain comprising a CD20-specific receptor. The
 CC genetically engineered CD20-specific redirected T cells are useful
 CC for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or
 CC CD20+ acute or chronic leukemia, in a human patient having previously
 CC undergone myeloablative chemotherapy and stem cell rescue. The
 CC genetically engineered CD20-specific redirected T cells are also
 CC useful for abrogating an untoward B cell function, such as autoimmune

CC disease (lupus or rheumatoid arthritis) in a patient.
 XX
 SQ Sequence 32 BP; 7 A; 9 C; 5 G; 8 T; 3 other;
 Query Match 100.0%; Score 32; DB 21; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.1e-10;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GGTGATATCGTKTCACACACATCTCCAGCAAT 32
 Db 1 GGTGATATCGTKTCACACACATCTCCAGCAAT 32
 RESULT 2
 AAK99179
 ID AAK99179 standard; DNA; 33 BP.
 CC
 XX AAK99179;
 DT
 XX 12-JUN-2002 (first entry)
 DE 33-mer oligonucleotide #4 related to the invention.
 KW Mouse monoclonal antibody; murine; surface antigen pres1 epitope;
 KW hepatitis B virus; PCR; primer; ss.
 XX Unidentified.
 OS
 XX KR99008647-A.
 PN
 XX 05-FEB-1999.
 PD
 XX 02-JUL-1997; 97KR-0030694.
 PF
 XX 02-JUL-1997; 97KR-0030694.
 PR
 XX (KORE-) KOREA RES INST CHEM TECHNOLOGY.
 PA
 XX Hong HJ, Ryoo CJ;
 PI
 XX WPI; 2000-168375/15.
 DR
 XX Changeable region of mouse monoclonal antibody recognizing surface
 PT antigen pres1 epitope of hepatitis B virus and gene -
 XX
 PS Disclosure; Page 7; 14pp; Korean.
 CC The invention relates to a changeable region of mouse monoclonal antibod
 CC recognising surface antigen pres1 epitope of hepatitis B virus and gene.
 CC This polynucleotide sequence relates to a 33-mer oligonucleotide of the
 CC invention.
 XX
 SQ Sequence 33 BP; 8 A; 9 C; 5 G; 8 T; 3 other;
 Query Match 71.9%; Score 23; DB 21; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 10 GTKCTCACACATCTCCAGCAAT 32
 Db 11 GTKCTCACACATCTCCAGCAAT 33
 RESULT 3
 ABK15810
 ID ABK15810 standard; DNA; 33 BP.
 CC
 XX ABK15810;
 AC
 XX 20-MAY-2002 (first entry)
 DT
 XX Mouse monoclonal antibody associated oligonucleotide #4.
 DE

Sequence 5, Appli
Sequence 30, Appl
Sequence 105, Appl
Sequence 50, Appl
Sequence 1782, Ap
Sequence 16986, A
Sequence 307, App
Sequence 2052, Ap

93 11 34.4 717 10 US-09-808-037-5
94 11 34.4 720 10 US-09-976-787-30
95 11 34.4 731 10 US-09-770-149-105
c 96 11 34.4 797 9 US-10-002-344A-50
97 11 34.4 797 10 US-09-764-864-1782
c 98 11 34.4 805 10 US-09-864-761-16986
c 99 11 34.4 807 12 US-10-062-254-307
c 100 11 34.4 838 10 US-09-974-300-2052

ALIGNMENTS

RESULT 1

US-09-832-292-44/c
; Sequence 44, Application US/09832292
; Patent No. US2002017205A1

GENERAL INFORMATION:

; APPLICANT: Rvazanov, Alexey
; TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF

FILE REFERENCE: 601-1-098CIP

; CURRENT APPLICATION NUMBER: US/09/832,292

; CURRENT FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 09/632,131

; PRIOR FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 44

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-09-832-292-44

Query Match 34.4%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32

Db 17 TCTCCAGCAAT 7

RESULT 2

US-09-864-864-166/c
; Sequence 166, Application US/09864864
; Patent No. US20020102679A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Secrist, Heather

; APPLICANT: Lodes, Michael J.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steve P.

; APPLICANT: Mannion, Jane

; APPLICANT: Benson, Darin R.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.523

; CURRENT APPLICATION NUMBER: US/09/864,864

; CURRENT FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 341

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 166

; LENGTH: 73

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-864-864-166

Query Match 34.4%; Score 11; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TCTCCAGCAAT 32

Db 35 TCTCCAGCAAT 25

RESULT 3

US-09-864-761-28949/c

; Sequence 28949, Application US/09864761

; Patent No. US20020048763A1

GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES U

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 28949

; LENGTH: 97

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC022843.3

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.54

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.54

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.56

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 25.561 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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13	11	34.4	318	4	US-09-344-050-104
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ALIGNMENTS

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; Sequence 46, Application US/08855910
; Patent No. 6221640
; GENERAL INFORMATION:
; APPLICANT: Tao, Jianshi
; APPLICANT: Sassanfar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Avruch, Anthony S.
; APPLICANT: Yu, Russell V.
; APPLICANT: Nair, Shamila
; TITLE OF INVENTION: ENTEROCOCCAL AMINOACYL-TRNA SYNTHETASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855.910
; FILING DATE: 14-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI95-08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-855-910-46

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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
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; Patent No. 587293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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; FILING DATE:
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; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
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US-08-449-287-21

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; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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GenCore version 5.1.3
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(without alignments)
1534.188 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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 TITLE Cd19xcd3 specific polypeptides and uses thereof
 JOURNAL Patent: WO 9954440-A 4 28-OCT-1999;
 RIETHMUELLER GERT (DE); BARGOU RALF (DE); DOERKEN BERND (DE); KUFER PETER (DE); LOEFFLER ANJA (DE); LUTTERBUESE RALF (DE)
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 Db 2 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGTCGTTTT 39
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 REFERENCE 1 (bases 1 to 445)
 AUTHORS Mueller-Hermelink,H.K., Greiner,A., Doerken,B., Bargou,R. and Kufer,P.
 TITLE Antibodies against plasma cells
 JOURNAL Patent: WO 0147953-A 16 05-JUL-2001;
 Mueller-Hermelink, Hans Konrad (DE); Greiner, Axel (DE)
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 VERSION AX083704.1 GI:13185432
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE 1 (bases 1 to 38)
 AUTHORS Arndt,M., Little,M., Kyriyanov,S., Krauss,J. and Pfreundschuh,M.
 TITLE F v? antibody construct comprising binding sites for a cd16
 receptor and a cd30 surface protein
 JOURNAL Patent: WO 0111059-A 5 15-FEB-2001;
 Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rech (DE)

FEATURES
 source Location/Qualifiers
 1..38
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"
 BASE COUNT 7 a 6 c 14 g 11 t
 ORIGIN

Query Match 84.2%; Score 32; DB 6; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGT 32
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RESULT 4
 A44949 LOCUS
 DEFINITION Sequence 5 from Patent WO9515382.
 A44949
 ACCESSION
 VERSION A44949.1 GI:2299535

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 11:05:29 ; Search time 1216 Seconds
(without alignments)
506.109 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38

Sequence: 1 ccagggggccagtgatagacaagcttcgggtcgtcttc 38

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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16: em_estom:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	55.3	598	13	BI104341
C 2	21	55.3	598	13	BI149725
C 3	21	55.3	632	10	BB637724
C 4	21	55.3	640	14	BQ109114
C 5	21	55.3	644	10	BE281961
C 6	21	55.3	666	10	BE368882

C 7	21	55.3	668	13	BI104472
C 8	21	55.3	676	10	BE369087
C 9	21	55.3	694	12	BF134274
C 10	21	55.3	723	21	BI107220
C 11	21	55.3	739	10	BE284158
C 12	21	55.3	745	12	BG871607
C 13	21	55.3	812	12	BF159752
C 14	21	55.3	829	13	BI107357
C 15	21	55.3	855	10	BE371942
C 16	21	55.3	892	12	BG518664
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C 22	20	52.6	819	20	BF136899
C 23	20	52.6	829	12	BF144014
C 24	20	52.6	885	12	BF162852
C 25	20	52.6	896	13	BF149320
C 26	20	52.6	916	12	BF163514
C 27	20	52.6	928	12	BF143867
C 28	19	50.0	604	12	BF140035
C 29	19	50.0	634	10	BE371032
C 30	19	50.0	670	12	BF141092
C 31	19	50.0	685	12	BF136104
C 32	19	50.0	709	13	BI149624
C 33	19	50.0	718	12	BF136279
C 34	19	50.0	748	12	BF136397
C 35	19	50.0	767	12	BF165456
C 36	19	50.0	771	12	BF140551
C 37	19	50.0	783	12	BF143757
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C 39	19	50.0	794	13	BI150371
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C 43	19	50.0	865	13	BI150936
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C 65	16	42.1	387	17	AQ218112
C 66	16	42.1	404	17	AQ218168
C 67	16	42.1	424	17	AZ259751
C 68	16	42.1	458	14	BQ016725
C 69	16	42.1	500	17	TA164F06Q
C 70	16	42.1	502	10	AV544501
C 71	16	42.1	502	17	AQ607976
C 72	16	42.1	504	17	BI1979
C 73	16	42.1	547	13	BI820445
C 74	16	42.1	568	17	AZ957414
C 75	16	42.1	568	17	AQ526730
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C 77	16	42.1	616	10	AV732984
C 78	16	42.1	652	12	BG526166
C 79	16	42.1	672	13	BJ274361

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90      16 42.1 1009 14 BO923184 AGENCOURT
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93      16 42.1 1239 14 BM914054 AGENCOURT
94      16 42.1 1985 11 BC017508 Homo sapi
95      15 39.5 85 10 BE226222 ia17b07.Y
96      15 39.5 142 9 AA614309 no77f09.s
97      15 39.5 148 12 BF084595 RC2-CT052
98      15 39.5 152 12 BF32952 IL3-HT061
99      15 39.5 154 9 AA038154 m178a07.r
100     15 39.5 193 10 BE654369 UT-M-AK1-

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ALIGNMENTS

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RESULT 1
BI104341/c
LOCUS
DEFINITION
602889919F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035013 5',
mRNA sequence.
ACCESSION
BI104341
VERSION
BI104341.1 GI:14555234
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 148 a 164 c 149 g 137 t
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FEATURES
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/organism="Mus musculus"
/strain="CZECH II"
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/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
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/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 148 a 164 c 149 g 137 t
ORIGIN
1 .598
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCAGGGCCAGTGATAGACA 21
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Db 501 CCAGGGCCAGTGATAGACA 481
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RESULT 2
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LOCUS
DEFINITION
602848572F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5012225 5',
mRNA sequence.
ACCESSION
BI149725
VERSION
BI149725.1 GI:14609726
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 598)
/organism="Mus musculus"
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/clone="IMAGE:5012225"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 140 a 165 c 151 g 142 t
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/organism="Mus musculus"
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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FEATURES
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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 140 a 165 c 151 g 142 t
ORIGIN
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/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5012225"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FEATURES
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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 140 a 165 c 151 g 142 t
ORIGIN
1 .598
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5012225"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
BB637724/c
LOCUS
DEFINITION
BB637724 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530093J23 5', mRNA sequence.
ACCESSION
BB637724
VERSION
BB637724.1 GI:16473475
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone="IMAGE:5035013"
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Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 148 a 164 c 149 g 137 t
ORIGIN
1 .598
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5035013"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
Query Match 55.3%; Score 21; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FT /label= VH6
FT misc_feature 260..277
FT /tag= b
FT /label= DN1
FT misc_feature 281..323
FT /tag= c
FT /label= JH4
FT misc_feature 324..414
FT /tag= d
FT /label= m-gamma-1

XX WO9634096-A1.
XX PD 31-OCT-1996.
XX FT 28-APR-1995; 95WO-US05500.
XX PR 28-APR-1995; 95WO-US05500.
XX PA (CELL-) CELL GENESYS INC.
XX PI Brenner DG, Capon DJ, Jakobovits A, Klapholz S,
XX Kucherlapati R;
XX DR WPI; 1996-497628/49.
XX FT Antibody contg. fully human variable region specifically reactive
XX PT with antigen - prepd. by immunisation of non-human animal incapable
XX PT of producing endogenous immunoglobulin (Ig), but capable of
XX PT producing human Ig
XX PS Example 7; Fig 16; 64pp; English.
XX CC The present sequence encodes the heavy chain of the anti-tetanus
XX CC toxin (TT) human monoclonal antibody (Mab) K4.1, which was secreted
XX CC by the hybridoma K4.1 obtained by immortalising B cells from
XX CC xenomice (containing integrated human DNA from the immunoglobulin
XX CC locus) immunised with TT. The Mab can be used for analysis,
XX CC diagnosis, research and therapy, particularly for human therapeutic,
XX CC and in vivo diagnostic applications.
XX SQ Sequence 414 BP; 98 A; 127 C; 98 G; 91 T; 0 other;

● Query Match 55.3%; Score 21; DB 17; Length 414;
● Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCAGGGGCCAGTGATAGACA 21
DB 364 CCAGGGGCCAGTGATAGACA 344

RESULT 6
AA57786/C
ID AA57786 standard; CDNA to mRNA; 447 BP.
XX AC AA57786;
XX DT 17-AUG-1999 (first entry)
XX DE Anti-HCV Ser/Thr protease Mab 8D4 heavy chain coding region.
XX KW Complementarity determining region; CDR; monoclonal antibody; Mab;
XX KW hepatitis C virus; HCV; protease; ds.
XX OS Mammalia.
XX PN JP1127861-A.
XX PI

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PD 18-MAY-1999.
XX XX
XX 29-OCT-1997; 97JP-0297451.
XX PF
XX 29-OCT-1997; 97JP-0297451.
XX PR
XX (NIHA ) JAPAN ENERGY CORP.
XX PA
XX WP1; 1999-350322/30.
XX DR P-PSDB; AAY14355.
XX PT Neutralized antibody partial peptide derived from hepatitis C virus
XX PT - useful for inhibiting Hepatitis C Virus (HCV) serine protease
XX PT activity
XX FT
XX Discloure; Page 17-18; 32pp; Japanese.
XX CC This sequence represents the coding region for the heavy chain of the
XX CC anti-HCV Ser/Thr protease Mab 8D4. The invention relates to the use
XX CC of partial peptides (AAV14348-Y14353) from the Mab 8D4 for inhibiting
XX CC HCV serine protease activity.
XX SQ Sequence 447 BP; 111 A; 115 C; 113 G; 108 T; 0 other;

Query Match 55.3%; Score 21; DB 20; Length 447;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCAGGGGCCAGTGATAGACA 21
DB 392 CCAGGGGCCAGTGATAGACA 372

RESULT 7
AAT59339/C
ID AAT59339 standard; CDNA; 486 BP.
XX AC AAT59339;
XX DT 21-AUG-1997 (first entry)
XX DE MH1 monoclonal antibody heavy chain encoding CDNA.
XX KW CDR; light chain; antigen binding site; antigen free animal;
XX KW germfree animal; immunoreactive; chromobotic event; ss.
XX OS Mus musculus.
XX FT
XX Key Location/Qualifiers
FH mat_peptide 1..486
FT /tag= a
FT /product= MH1_heavy_chain
FT misc_feature 82..96
FT /tag= b
FT /label= encodes_CDR1
FT misc_feature 139..189
FT /tag= c
FT /label= encodes_CDR2
FT misc_feature 286..321
FT /tag= d
FT /label= encodes_CDR3

XX WO9640986-A1.
XX PD 19-DEC-1996.
XX PF 29-APR-1996; 96WO-US07891.
XX PR 07-JUN-1995; 95US-0486420.
XX PA (AMBI-) AMERICAN BIOGENETIC SCI INC.
XX PI Dimitrijevic N, Dimitrijevic N;

```

CC chemotherapeutic agents. This sequence encodes the Wu-1 antibody
CC variable region heavy chain fragment described in the method of the
CC invention.
XX
SQ Sequence 445 BP; 108 A; 109 C; 124 G; 104 T; 0 other;
Query Match 100.0%; Score 38; DB 22; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTGTTT 38
DB 425 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTGTTT 388
RESULT 3
AAF61154
ID AAF61154 standard; DNA; 38 BP.
XX
AC AAF61154;
XX
DT 18-MAY-2001 (first entry)
XX
DE Single chain Fv antibody construct A9 VH domain PCR primer VH3.
XX
KW Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
KW tumor cell; natural killer cell activation; Hodgkin's disease;
KW Reed-Sternberg disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN DE1937264-A1.
XX
PD 15-FEB-2001.
XX
PF 06-AUG-1999; 99DE-1037264.
XX
PR 06-AUG-1999; 99DE-1037264.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;
XX WPI; 2001-184000/19.
XX
DR New Fv-antibody construct, useful for treating Hodgkin and
XX Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30
XX surface protein
XX
PS Example 1; Page 11; 18pp; German.
XX
CC This invention describes a novel Fv-antibody construct (I) having binding
XX sites for a CD16 receptor and a CD30 surface protein. The invention also
XX describes (1) expression vector encoding (I); (2) transformants
XX containing the vector of (1); (3) preparation of (I) by culturing cells
XX of (2); and (4) kit comprising (I) and/or the vector of (1), and
XX auxiliaries such as buffers, solvents, carriers, controls and labels, or
XX their replacements. The products of the invention have cytostatic
XX activity. (I) causes lysis of CD30+, specifically tumor, cells. It
XX activates natural killer cells, through the CD16 receptor, and directs
XX them to CD30-expressing cells. (I) are used to treat diseases in which
XX CD30+ cells are implicated, particularly tumors and specifically Hodgkin
XX or Reed-Sternberg diseases. (I) have a stronger lytic action than known
XX bispecific antibodies, can be produced on a large scale with high purity,
XX and contain no components that can induce unwanted immune responses.
XX
SQ Sequence 38 BP; 7 A; 6 C; 14 G; 11 T; 0 other;
Query Match 84.2%; Score 32; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 425 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTGTTT 388
RESULT 4
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ID AAF61154 standard; DNA; 30 BP.
XX
AC AAX89880;
XX
DT 18-OCT-1999 (first entry)
XX
DE Monoclonal antibody 8E5 Vh chain amplifying 3' primer.
XX
KW Fibrin; monoclonal antibody; MAb; 8E5; thrombosis; human;
KW thrombolytic disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CN1195701-A.
XX
PD 14-OCT-1998.
XX
PF 08-APR-1997; 97CN-0103756.
XX
PR 08-APR-1997; 97CN-0103756.
XX
PA (HEAM-) HEAMTOLOGY INST CHINESE ACAD SCI.
XX
PI Song Z;
XX
DR WPI; 1999-096572/09.
XX
PT Anti-human fibrin monoclonal antibody heavy chain and light chain
PT variable region gene - useful in thrombolytic medicine
XX
PS Example 2; Page 5; 16pp; Chinese.
XX
CC The invention provides a gene encoding light and heavy chain variable
XX regions of an anti-human fibrin monoclonal antibody (MAB). The gene is
XX used in the preparation of a diagnostic reagent for diagnosis of
XX thrombosis and in treatment of thrombolytic disorders. Sequences
XX CC AAX89879-80 represents PCR primers for amplifying the cDNA encoding the
XX Vh chain of MAb 8E5.
XX
SQ Sequence 30 BP; 5 A; 4 C; 11 G; 10 T; 0 other;
Query Match 71.1%; Score 27; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TGGATAGACAAAGCTTGGGTGCTGTTT 38
DB 1 TGGATAGACAAAGCTTGGGTGCTGTTT 27
RESULT 5
AAT38697/c
ID AAT38697 standard; cDNA; 414 BP.
XX
AC AAT38697;
XX
DT 01-JUL-1997 (first entry)
XX
DE Anti-tetanus toxin human monoclonal antibody K4.1 heavy chain cDNA.
XX
KW Heavy chain; tetanus; toxin; human; monoclonal; antibody; K4.1;
KW hybridoma; immortalisation; in vivo; xenomice; analysis;
KW immunoglobulin; diagnosis; research; therapy; B cell; ss.
XX
OS Homo sapiens.

QY 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTGTTT 32
DB 1 CCAGGGCCAGTGGATAGACAAAGCTTGGGTGCTGTTT 32
RESULT 4
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ID AAX89880 standard; DNA; 30 BP.
XX
AC AAX89880;
XX
DT 18-OCT-1999 (first entry)
XX
DE Monoclonal antibody 8E5 Vh chain amplifying 3' primer.
XX
KW Fibrin; monoclonal antibody; MAb; 8E5; thrombosis; human;
KW thrombolytic disorder; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CN1195701-A.
XX
PD 14-OCT-1998.
XX
PF 08-APR-1997; 97CN-0103756.
XX
PR 08-APR-1997; 97CN-0103756.
XX
PA (HEAM-) HEAMTOLOGY INST CHINESE ACAD SCI.
XX
PI Song Z;
XX
DR WPI; 1999-096572/09.
XX
PT Anti-human fibrin monoclonal antibody heavy chain and light chain
PT variable region gene - useful in thrombolytic medicine
XX
PS Example 2; Page 5; 16pp; Chinese.
XX
CC The invention provides a gene encoding light and heavy chain variable
XX regions of an anti-human fibrin monoclonal antibody (MAB). The gene is
XX used in the preparation of a diagnostic reagent for diagnosis of
XX thrombosis and in treatment of thrombolytic disorders. Sequences
XX CC AAX89879-80 represents PCR primers for amplifying the cDNA encoding the
XX Vh chain of MAb 8E5.
XX
SQ Sequence 30 BP; 5 A; 4 C; 11 G; 10 T; 0 other;
Query Match 71.1%; Score 27; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 TGGATAGACAAAGCTTGGGTGCTGTTT 38
DB 1 TGGATAGACAAAGCTTGGGTGCTGTTT 27
RESULT 5
AAT38697/c
ID AAT38697 standard; cDNA; 414 BP.
XX
AC AAT38697;
XX
DT 01-JUL-1997 (first entry)
XX
DE Anti-tetanus toxin human monoclonal antibody K4.1 heavy chain cDNA.
XX
KW Heavy chain; tetanus; toxin; human; monoclonal; antibody; K4.1;
KW hybridoma; immortalisation; in vivo; xenomice; analysis;
KW immunoglobulin; diagnosis; research; therapy; B cell; ss.
XX
OS Homo sapiens.

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:54 ; Search time 153.159 Seconds
(without alignments)
558,741 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	C	21	55.3	699	22	AAH7715
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Coding sequence fo
Monoclonal antibody
6D9 antibody heavy
Antibody 3G2 heavy
IgG Fab-BPI fusion
Mouse antibody H3-
Mouse antibody FB3
Murine ASB57 Fd fr
WOW-1 Fab heavy ch
Sequence of clone
Fd phage clone seq
Sequence of PCR pr
Murine Mab SK48-E2
Human penton base
Heavy chain of ant
Sequence encoding
Murine anti-BGH MA
Anti-DOH monoclon
Sequence encoding
Anti-Fas Mab HFE7A
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Murine anti-Fas an
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Humanised anti-Fas
DNA encoding TPA-8
Glycophorin antibo
Human B7.1-murine
Human penton base
Combined cDNA inse
mRNA encoding gam
Anti-tobacco mosai
Mab 55.1 heavy cha
Murine anti-potuli
Murine anti-potuli
Murine anti-potuli
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IAS MBP 90-101 CH1
Mouse 6D9 catalyri
3B1 single chain a
Mouse immunoglobul
Newborn mouse immu
Mouse immunoglobul
Plasmd pUC19/muA5
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IAS MBP 1-14 CH1.C
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Murine anti-potuli
Alpha-lactalbumin
Alpha-lactalbumin
Alpha-lactalbumin
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LMBOTC vector #1.
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AD7 and 5C6 heavy
Gamma1 gene CH1 re
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Anti-RSV F protein
Anti-erbA2 antibody
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Light chain of an
Heavy chain of an
Recombinant 4G10 a
Sequence of mouse
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 29.6585 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38

Sequence: 1 ccaggggcccagtcgagacagccttgcgtcttc 38

Scoring table: OLIGO_NUC
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Wo ze : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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C 16	20	52.6	2059	10	US-09-815-837-66
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C 83	14	36.8	32190	9	US-09-860-670-255	Sequence 255, Appl
C 84	14	36.8	32249	9	US-09-860-670-260	Sequence 260, Appl
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C 91	13	34.2	39	10	US-09-854-811-26	Sequence 26, Appl
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c 95 13 34.2 114 9 US-09-232-880-161 Sequence 161, App
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ALIGNMENTS

RESULT 1

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; Patent No. US20020132983A1

GENERAL INFORMATION:

; APPLICANT: Junghans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti

; FILE REFERENCE: 003

; CURRENT APPLICATION NUMBER: US/10/006,773

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/250,089

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 12

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; TYPE: DNA

; ORGANISM: Mus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (14)..(430)

; OTHER INFORMATION: 4D4 Heavy chain V region, plus leader

US-10-006-773-12

Query Match 55.3%; Score 21; DB 12; Length 736;

Best Local Similarity 100.0%; Pred. No. 0.0056;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21

Db 471 CCAGGGCCAGTGGATAGACA 451

RESULT 2

US-09-903-327A-5/c

; Sequence 5, Application US/09903327A

; Patent No. US2002016433A1

GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Eryuang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; TITLE OF INVENTION: GENE

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1314

; TYPE: DNA

; ORGANISM: Mouse

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (0)..(1314)

; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein

; OTHER INFORMATION: bifunctional antibody

US-09-903-327A-5

Query Match 55.3%; Score 21; DB 9; Length 1314;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21

Db 437 CCAGGGCCAGTGGATAGACA 417

RESULT 3

US-09-910-059-130/c

; Sequence 130, Application US/09910059

; Patent No. US20020142359A1

GENERAL INFORMATION:

; APPLICANT: Copley, Clive G

; APPLICANT: Emery, Stephen Charles

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

; FILE REFERENCE: 1991-209

; CURRENT APPLICATION NUMBER: US/09/910,059

; CURRENT FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 09/171,945

; PRIOR FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: PCT/GB97/01165

; PRIOR FILING DATE: 1997-04-29

; PRIOR APPLICATION NUMBER: GB 9703103.3

; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7

; PRIOR FILING DATE: 1996-05-04

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 130

; LENGTH: 1446

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (16)..(1434)

; OTHER INFORMATION:

US-09-910-059-130

Query Match 55.3%; Score 21; DB 10; Length 1446;

Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21

Db 1145 CCAGGGCCAGTGGATAGACA 1125

RESULT 4

US-09-903-327A-1/c

; Sequence 1, Application US/09903327A

; Patent No. US2002016433A1

GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Eryuang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; TITLE OF INVENTION: GENE

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1516

; TYPE: DNA

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 30.3537 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-10

Perfect score: 38
Sequence: 1 ccaggggcccagtgatagacaagcttgggtcgtctttc 38

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA: *
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6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C	21	55.3	411	2	US-08-331-397B-57	Sequence 57, Appl	
C	21	55.3	411	2	US-08-759-804A-56	Sequence 56, Appl	
5	21	55.3	636	2	US-08-737-129A-1	Sequence 1, Appl	
C	6	21	55.3	645	4	US-09-170-769A-5	Sequence 5, Appl
C	7	21	55.3	666	2	US-08-737-129A-5	Sequence 5, Appl
C	8	21	55.3	717	5	PCT-US94-14106-58	Sequence 58, Appl
9	21	55.3	735	5	PCT-US94-14106-50	Sequence 50, Appl	
C	10	21	55.3	777	2	US-08-860-882A-25	Sequence 25, Appl
C	11	21	55.3	777	4	US-09-011-769A-20	Sequence 20, Appl
C	12	21	55.3	798	1	US-08-133-011-99	Sequence 99, Appl
C	13	21	55.3	798	1	US-08-332-730A-99	Sequence 99, Appl
C	14	21	55.3	798	1	US-08-387-874-71	Sequence 71, Appl
C	15	21	55.3	798	1	US-08-383-619-99	Sequence 99, Appl
C	16	21	55.3	798	4	US-08-907-739-99	Sequence 99, Appl
C	17	21	55.3	798	4	US-09-729-597-99	Sequence 99, Appl
C	18	21	55.3	798	5	PCT-US93-08364-71	Sequence 71, Appl
C	19	21	55.3	830	1	US-08-133-011-115	Sequence 115, Appl
C	20	21	55.3	830	1	US-08-332-730A-115	Sequence 115, Appl
C	21	55.3	830	1	US-08-387-874-88	Sequence 88, Appl	
C	22	21	55.3	830	2	US-08-383-619-115	Sequence 115, Appl
C	23	21	55.3	830	4	US-08-907-739-115	Sequence 115, Appl
C	24	21	55.3	830	4	US-09-729-597-115	Sequence 115, Appl
C	25	21	55.3	830	5	PCT-US93-08364-88	Sequence 88, Appl
C	26	21	55.3	923	5	PCT-US94-07659-1	Sequence 1, Appl
C	27	21	55.3	1347	6	5455030-2	Patent No. 5455030

C	28	21	55.3	1443	2	US-08-403-853-19	Sequence 19, Appl
C	29	21	55.3	1446	4	US-09-171-945-130	Sequence 130, App
C	30	21	55.3	1572	1	US-08-353-400-23	Sequence 23, Appl
C	31	21	55.3	1632	2	US-08-792-824-8	Sequence 8, Appl
C	32	21	55.3	1641	2	US-08-792-824-5	Sequence 5, Appl
C	33	21	55.3	1644	2	US-08-792-824-11	Sequence 11, Appl
C	34	21	55.3	1672	2	US-08-792-824-2	Sequence 2, Appl
C	35	21	55.3	1797	1	US-08-442-542-17	Sequence 17, Appl
C	36	21	55.3	1797	3	US-08-765-466-17	Sequence 17, Appl
C	37	21	55.3	1800	2	US-08-579-940-6	Sequence 6, Appl
C	38	21	55.3	1974	4	US-09-423-439-59	Sequence 59, Appl
C	39	21	55.3	3343	6	5453363-2	Patent No. 5453363
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C	41	20	52.6	27	1	US-08-061-092A-6	Sequence 6, Appl
C	42	20	52.6	27	1	US-08-290-592E-1	Sequence 1, Appl
C	43	20	52.6	27	5	PCT-US95-10053-1	Sequence 1, Appl
C	44	20	52.6	27	5	PCT-US96-09448-1	Sequence 1, Appl
C	45	20	52.6	690	2	US-08-634-783A-1	Sequence 1, Appl
C	46	20	52.6	690	3	US-09-070-817-1	Sequence 1, Appl
C	47	19	50.0	19	1	US-08-167-336A-9	Sequence 9, Appl
C	48	19	50.0	19	1	US-08-416-962-9	Sequence 9, Appl
C	49	19	50.0	19	1	US-08-589-011-9	Sequence 9, Appl
C	50	19	50.0	19	2	US-08-948-762-9	Sequence 9, Appl
C	51	19	50.0	23	2	US-08-465-473B-20	Sequence 20, Appl
C	52	19	50.0	28	1	US-07-977-696C-3	Sequence 3, Appl
C	53	19	50.0	28	1	US-08-129-930B-3	Sequence 3, Appl
C	54	19	50.0	28	4	US-08-976-288A-3	Sequence 3, Appl
C	55	19	50.0	524	5	PCT-US91-02942-4	Sequence 4, Appl
C	56	19	50.0	1570	2	US-08-303-562B-6	Sequence 6, Appl
C	57	19	50.0	1570	2	US-08-116-247-6	Sequence 6, Appl
C	58	18	47.4	18	4	US-09-199-149-18	Sequence 18, Appl
C	59	18	47.4	693	2	US-08-634-783A-3	Sequence 3, Appl
C	60	18	47.4	693	3	US-09-070-817-3	Sequence 3, Appl
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C	62	17	44.7	24	2	US-08-331-397B-5	Sequence 5, Appl
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C	66	17	44.7	28	1	US-08-436-717-23	Sequence 23, Appl
C	67	17	44.7	28	2	US-08-553-501A-25	Sequence 25, Appl
C	68	17	44.7	28	2	US-08-765-783A-25	Sequence 25, Appl
C	69	17	44.7	28	3	US-08-921-100-25	Sequence 25, Appl
C	70	17	44.7	28	3	US-08-880-141-25	Sequence 25, Appl
C	71	17	44.7	28	3	US-08-902-201-25	Sequence 25, Appl
C	72	17	44.7	28	3	US-09-205-231-25	Sequence 25, Appl
C	73	17	44.7	28	4	US-08-646-265A-25	Sequence 25, Appl
C	74	17	44.7	28	4	US-09-416-557-25	Sequence 25, Appl
C	75	17	44.7	29	1	US-08-442-542-40	Sequence 40, Appl
C	76	17	44.7	29	3	US-08-765-466-40	Sequence 40, Appl
C	77	17	44.7	34	1	US-08-442-542-49	Sequence 49, Appl
C	78	17	44.7	34	3	US-08-765-466-49	Sequence 49, Appl
C	79	17	44.7	470	2	US-08-561-521-3	Sequence 3, Appl
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C	81	16	42.1	54	5	PCT-US96-10905-17	Sequence 17, Appl
C	82	15	39.5	15	1	US-08-290-592E-3	Sequence 3, Appl
C	83	15	39.5	15	5	PCT-US96-09448-3	Sequence 3, Appl
C	84	15	39.5	23	2	US-08-303-562B-2	Sequence 2, Appl
C	85	15	39.5	23	2	US-08-070-116A-16	Sequence 16, Appl
C	86	15	39.5	23	2	US-08-116-247-2	Sequence 2, Appl
C	87	15	39.5	360	1	US-08-447-422-14	Sequence 14, Appl
C	88	15	39.5	419	4	US-09-214-095D-89	Sequence 89, Appl
C	89	15	39.5	735	5	PCT-US94-14106-54	Sequence 54, Appl
C	90	15	39.5	765	2	US-07-690-192-3	Sequence 3, Appl
C	91	15	39.5	856	4	US-09-535-008-55	Sequence 55, Appl
C	92	15	39.5	1440	2	US-08-224-482-5	Sequence 5, Appl
C	93	15	39.5	1448	1	US-08-447-422-15	Sequence 15, Appl
C	94	15	39.5	2811	1	US-08-040-548-31	Sequence 31, Appl
C	95	15	39.5	2811	1	US-08-466-344-31	Sequence 31, Appl
C	96	15	39.5	2817	6	5206152-6	Patent No. 5206152
C	97	14	36.8	449	4	US-08-688-908-3	Sequence 3, Appl
C	98	14	36.8	454	2	US-08-737-560A-6	Sequence 6, Appl
C	99	14	36.8	498	1	US-07-781-254A-14	Sequence 14, Appl
C	100	14	36.8	1218	1	US-08-351-473B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-353-400-5
; Sequence 5, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353.400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-353-400-5

Query Match 55.3%; Score 21; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21
|||
Db 5 CCAGGGCCAGTGGATAGACA 25

RESULT 2
US-08-331-398A-57/c
; Sequence 57, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.398A

; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..411
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B1 Fv
; Heavy chain region"
US-08-331-398A-57

Query Match 55.3%; Score 21; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGGGCCAGTGGATAGACA 21
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Db 404 CCAGGGCCAGTGGATAGACA 384

RESULT 3
US-08-331-397B-57/c
; Sequence 57, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; Specific Antibody Fragments, Fusion Proteins, and U
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and U
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:55:54 ; Search time 720.841 Seconds

(without alignments)
1534.188 Million cell updates/sec

Title: US-09-424-705B-11

Perfect score: 38
Sequence: 1 cagccgcatggcgaggtscagctgcagsgagtcwgg 38Scoring table: OLIGO_NUC
Gapop 60.0 , Gapect 60.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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33: em_hcg_mus:*
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41: em_hcgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	20	52.6	1653	6	AX011208 Sequence
6	20	52.6	1698	6	AX011206 Sequence
7	20	52.6	4072	12	ASY12737 Artificial
8	17	44.7	56	6	AX167798 Sequence
9	17	44.7	348	6	A76070 Sequence 9
10	17	44.7	348	10	MM1GHCVR
11	17	44.7	445	6	AX190429 Sequence
12	17	44.7	689	9	HSJ32193 Sequence
13	17	44.7	3970	12	ASY14585 Artificial
14	17	44.7	3991	12	ASY12778 Artificial
15	17	44.7	4354	12	ASY14583 Artificial
16	17	44.7	4363	12	SCFV18290
17	17	44.7	4864	12	ASY14584 Artificial
18	17	44.7	10029	12	AE011972
19	17	44.7	230685	2	AL390719 Xanthomon
20	17	44.7	345783	1	AP003001 Mesorhizo
21	16	42.1	684	6	AX421599 Sequence
22	16	42.1	909	10	AF035208 Mus muscu
23	16	42.1	999	10	BC009810 Mus muscu
24	16	42.1	1332	6	AR116877 Sequence
25	16	42.1	1332	6	AR175870 Sequence
26	16	42.1	1350	12	AF353576 Synthetic
27	16	42.1	1515	6	AR116878 Sequence
28	16	42.1	1515	6	AR175871 Sequence
29	16	42.1	1515	6	AB022700 Aspergill
30	16	42.1	1590	8	AY013315 Aspergill
31	16	42.1	2363	6	AR018076 Sequence
32	16	42.1	2363	6	AR051916 Sequence
33	16	42.1	2379	8	AR053934 Sequence
34	16	42.1	2379	8	ASNPHTAS
35	16	42.1	10029	1	AE012501 Xanthomon
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40	16	42.1	11252	1	AE012008 Xanthomon
41	16	42.1	11272	1	AE009043 Agrobacte
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43	16	42.1	15773	1	AE004958 Pseudomon
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51	16	42.1	134962	8	AP003279 Oryza sat
52	16	42.1	144520	2	AP004278 Oryza sat
53	16	42.1	150450	2	AC121489 Oryza sat
54	16	42.1	151502	8	OSJN00080 Oryza sat
55	16	42.1	162774	8	OSJN00105 Oryza sat
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58	16	42.1	340900	1	SMES91791 Sinothizo
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62	15	39.5	703	6	AB6012 Sequence 67
63	15	39.5	703	6	AR155505 Sequence
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78 15 39.5 2097 10 AF037313
79 15 39.5 2147 8 NCNURI
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91 15 39.5 7617 6 AX024252
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99 15 39.5 10676 1 AE012538
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AE011875 Xanthomon

ALIGNMENTS

RESULT 1
AX014264
LOCUS
DEFINITION Sequence 3 from Patent WO9954440.
ACCESSION AX014264
VERSION AX014264.1 GI:10040639
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Bargou,R., Kufer,P., Loeffler,A. and Lutterbuesse,R.
TITLE Cdl9xcd3 specific polypeptides and uses thereof
JOURNAL Patent: WO 9954440-A 3 28-OCT-1999;
RIETHMUELLER GERT (DE); BARGOU RALF (DE); DOERKEN BERND (DE); KUFER PETER (DE); LOEFFLER ANJA (DE); LUTTERBUESSE RALF (DE)
FEATURES
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAGCGGGCCATGGCGCAGGTSCAGTGCAGSAG 33

RESULT 2
AX011221
LOCUS
DEFINITION Sequence 16 from Patent WO9957150.
ACCESSION AX011221
VERSION AX011221.1 GI:9997801
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kipriyanov,S. and Little,M.
TITLE Multivalent antibody constructs
JOURNAL Patent: WO 9957150-A 16 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
FEATURES
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Location/Qualifiers
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LOCUS
DEFINITION Sequence 4 from Patent WO011059.
ACCESSION AX083703
VERSION AX083703.1 GI:13185431
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 35)
AUTHORS Arndt,M., Little,M., Kypriyanov,S., Krauss,J. and Pfreundschuh,M.
TITLE F v? antibody construct comprising binding sites for a cd16 receptor and a cd30 surface protein
JOURNAL Patent: WO 011059-A 4 15-FEB-2001;
Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rech (DE)
FEATURES
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RESULT 4
AF148718
LOCUS
DEFINITION Synthetic construct single chain anti-transferrin receptor antibody-streptavidin fusion protein mRNA, complete cds.
ACCESSION AF148718


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99 15 39.5 609 13 BI351055
100 15 39.5 612 10 AW424743

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ALIGNMENTS

```

RESULT 1
BB564459/c 290 bp mRNA linear EST 29-NOV-2000
LOCUS BB564459 RIKEN full-length enriched, adult male small intestine Mus
DEFINITION musculus CDNA clone 2010014G07 5', mRNA sequence.
ACCESSION BB564459
VERSION BB564459.1 GI:11455351
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 290)
AUTHORS Hanagaki, T., Hayashi, Y., Itoh, M., Iwata, T., Hirozane, T., Hodojima, Y.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno
H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K.,
Nomura, K., Numazaki, D., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,
Sakai, K., Sakai, K., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,
Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka
T., Taya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermocyclization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for

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further details. Location/Qualifiers
1..290
/organism="Mus musculus"
/db_xref="taxon:10090"
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/dev stage="adult"
/lab host="SOLR"
/notes="Site_1: XhoI; Site_2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCGCGCCCACTCGAGTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 20.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGCGCGCCCACTCGAGTCTTTTCTTTT 3']. cDNA was
3']. cDNA was cleaved with XhoI and SstI."
BASE COUNT 82 a 79 c 84 g 45 t
ORIGIN
Query Match 42.1%; Score 16; DB 10; Length 290;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CGGCCATGGCGCAGGT 20
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LOCUS BF226545 NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:3672445 5'
DEFINITION similar to TR:Q92P7 Q92P7 GES30. i, mRNA sequence.
ACCESSION BF226545
VERSION BF226545.1 GI:11134311
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 348)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue procurement: Jeffrey Green M.D.
cDNA library preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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Location/Qualifiers
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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558.741 Million cell updates/sec

Title: US-09-424-705B-11

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Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

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Minimum DB seq length: 0

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SUMMARIES

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2	23	60.5	32	21	AAK99182
3	23	60.5	32	21	ABK15813
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5	20	52.6	33	21	AAZ43426
6	20	52.6	35	22	AAE61153
7	20	52.6	898	19	AAV73335
8	20	52.6	1653	21	AAZ43432
9	20	52.6	1698	21	AAZ43431

10	20	52.6	1794	19	AAV73337
11	18	47.4	2031	21	AAAI3527
12	17	44.7	56	22	AAH25553
13	17	44.7	348	13	AAQ22736
14	17	44.7	348	14	AAQ49376
15	17	44.7	445	22	AAH21233
16	16	42.1	22	21	AAAI5023
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18	16	42.1	684	22	ABU01494
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22	16	42.1	2363	15	AAQ58126
23	16	42.1	2379	34	AAQ65944
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33	15	39.5	978	22	AAQ30728
34	15	39.5	993	21	AAAI3528
35	15	39.5	1100	21	AAQ44049
36	15	39.5	1173	18	AAQ61867
37	15	39.5	1173	21	AAQ39799
38	15	39.5	1332	18	AAQ67087
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40	15	39.5	2199	22	AAQ30727
41	15	39.5	4570	22	AAQ61152
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43	14	36.8	20	18	AAQ61192
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45	14	36.8	21	21	AAQ58680
46	14	36.8	21	21	AAZ43496
47	14	36.8	21	21	AAZ43458
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49	14	36.8	22	13	AAQ23579
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53	14	36.8	22	13	AAQ28657
54	14	36.8	22	13	AAQ30564
55	14	36.8	22	13	AAQ32770
56	14	36.8	22	14	AAQ34933
57	14	36.8	22	14	AAQ36936
58	14	36.8	22	14	AAQ49620
59	14	36.8	22	15	AAQ62522
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Mouse bispecific a
Phagemid ph7 gene
Primer used to amp
RSV9 VH. Mus mus
RSV9 heavy chain
Murine derived ant
PCR primer VHB13c
Human ORFX polyom
Murine apoptosis r
Aspergillus niger
Carot. extensin le
Aspergillus niger
Phyase gene. Asp
A. niger phyase g
1.1ASML VHBAC o1
Primer HUVH2. NCO f
Human V gene 11bra
Human V gene 11bra
Human V gene 11bra
Human V gene 11bra
Murine metallochio
General Pab PCR pr
Antibody 8860 biva
Anti-FIX/Fix anti
Phagemid ph17 fusi
Zea mays DNA fragm
Mouse ATP sensitiv
DNA sequence of mo
Mouse k-ATP channe
Mouse ATP-sensitiv
Anti-FIX/Fix anti
Single chain Fv an
Acetobacter xylinu
Primer VH2 for hea
Human immunoglobul
Primer VH1BACK. S
Human antibody hea
Human antibody hea
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Fusion antibody pr
Primer VHB1BACK. S
Primer VHB1BACK. S
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Primer VHB1. Syn
VHB1BACK primer to
mum4b45 heavy cha
PCR primer VHB1BACK
PCR primer for amp
Primer used in con
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VH chain cDNA PCR
PCR primer VHB1BACK
PCR primer VHB1BACK
HP1/2 PCR primer V
Heavy chain PCR pr
Mouse anti-KiH VH
Primer VHB1BACK bas
Mouse derived VH R
Ig heavy chain vari
Heavy chain variab
Murine VH conserve
Primer VHB1AC for
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OMV10 heavy chain
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Mouse heavy chain
Primer VHB1BACK for
Murine monoclonal
Primer VHB1BACK for
Immunoglobulin con

83 VH1BACK primer for
84 Primer for amplify
85 Primer VH1BACK for
86 Construction of tr
87 Primer RVH-1BACK f
88 Murine MAB B7 heav
89 RT-PCR primer VH1B
90 PCR primer, VH1BAC
91 Primer PCR.51 used
92 PCR primer for hea
93 Human sialic acid
94 PCR primer 1. Syn
95 MAB FC-2.15 V regi
96 Ing of pluck2001 P
97 Monoclonal antibod
98 PCR primer for lla
99 Llama antibody hea
100 Llama HC-V domain

ALIGNMENTS

RESULT 1
AAZ30326 AAZ30326 standard; DNA; 33 BP.
XX
AC AAZ30326;
XX
DT 11-FEB-2000 (first entry)
XX
DE PCR primer 5'H1 used to amplify the variable heavy chain domain.
XX
KW Variable heavy chain domain; HD37 hybridoma; bscCD19xCD3 antibody;
KW bispecific single-chain fragment; CD19 antigen; CD3 antigen;
KW CD19-positive target cell; T-cell stimulation; cytotoxic T-lymphocyte;
KW B-cell malignancy; B-cell mediated autoimmune disease; myasthenia gravis;
KW Morbus Basedow; Hashimoto thyroiditis; Goodpasture syndrome;
KW B-cell depletion; non-Hodgkin lymphoma; gene therapy; cancer;
KW viral disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO9954440-A1.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-EP02693.
PF
XX
XX 21-APR-1998; 98EP-0107269.
PR
XX
XX (DOER/) DOERKEN B.
PA
XX (RIET/) RIETHMUELLER G.
PA
XX
XX Kufer P, Lutterbuese R, Bargou R, Loeffler A;
PI
XX
XX WPI; 2000-013241/01.
DR
XX
XX Novel multifunctional polypeptide for treating B-cell malignancies
PT especially non-Hodgkin lymphoma -
PT
XX
XX Example 1; Page 33; 91pp; English.
PS
XX
XX PCR primers AAZ30326-27 were used to amplify the variable heavy chain
CC domain from the HD37 hybridoma. The amplified sequence was cloned and
CC used to produce bispecific single-chain fragments, specifically a
CC bscCD19xCD3 antibody, comprising domains providing binding-site of
CC immunoglobulin chains or antibodies specifically recognizing CD19 and
CC CD3 antigen. The polypeptide destroys CD19-positive target cells without
CC any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic
CC T-lymphocytes and so specific lysis by T-cells rather than a direct
CC effect by an antibody is achieved. The bispecific single-chain
CC fragments, or nucleotides encoding them, are used for the treatment of

CC B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia
CC gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome
CC or for the depletion of B- cells and more particularly non-Hodgkin
CC lymphoma in mammals preferably human. They can also delay the
CC pathological conditions caused by these diseases, and can be used
CC for detecting these diseases. The polynucleotide is used for gene
CC therapy. The polypeptides are also used for identifying compounds
CC modulating B-cell/T-cell mediated immune response with can in turn be
CC used for treating cancer, its related diseases and also for inhibiting
CC viral diseases by preventing viral infection.
XX
SQ Sequence 33 BP; 6 A; 10 C; 12 G; 3 T; 2 other;
Query Match 86.8%; Score 33; DB 21; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCGCCATGGCGCAGGTCAGCTGCAGSAG 33
Db 1 CAGCCGCCATGGCGCAGGTCAGCTGCAGSAG 33
RESULT 2
AAK99182
ID AAK99182 standard; DNA; 32 BP.
XX
AC AAK99182;
XX
DT 12-JUN-2002 (first entry)
XX
DE 32-mer oligonucleotide #7 related to the invention.
XX
KW Mouse monoclonal antibody; murine; surface antigen pres1 epitope;
KW hepatitis B virus; PCR; primer; ss.
XX
XX Unidentified.
OS
PN KR99008647-A.
XX
PD 05-FEB-1999.
XX
XX 02-JUL-1997; 97KR-0030694.
PF
XX
XX 02-JUL-1997; 97KR-0030694.
PR
XX
XX (KORE-) KOREA RES INST CHEM TECHNOLOGY.
PA
XX
XX Hong HJ, Ryoo CJ;
PI
XX
XX WPI; 2000-168375/15.
DR
XX
XX Changeable region of mouse monoclonal antibody recognizing surface
PT antigen pres1 epitope of hepatitis B virus and gene -
PT
XX
XX Disclosure; Page 8; 14pp; Korean.
PS
XX
XX The invention relates to a changeable region of mouse monoclonal antibody
CC recognising surface antigen pres1 epitope of hepatitis B virus and gene.
CC This polynucleotide sequence relates to a 32-mer oligonucleotide of the
CC invention.
XX
SQ Sequence 32 BP; 7 A; 6 C; 10 G; 6 T; 3 other;
Query Match 60.5%; Score 23; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 CAGGTCAGCTGCAGSAGTCWGG 38
Db 10 CAGGTCAGCTGCAGSAGTCWGG 32
RESULT 3

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:58 ; Search time 29.6585 Seconds
(without alignments)
563.882 Million cell updates/sec

Title: US-09-424-705B-11

Perfect score: 38
Sequence: 1 cagcgccatgagcgaggtscagctgcagagtcwag 38

Scoring table: OLIGO_NUC
Gapco 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Wo ze : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications_NA:*

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16	42.1	1515	10	US-09-929-060-5
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4	14	36.8	22	10	US-09-742-693-13
5	14	36.8	22	10	US-09-742-693-19
6	14	36.8	22	10	US-09-217-2688-10
7	14	36.8	22	10	US-09-910-059-6
8	14	36.8	45	9	US-09-293-854-20
9	14	36.8	45	10	US-09-893-615-68
10	14	36.8	45	10	US-09-893-615-69
11	14	36.8	45	10	US-09-893-615-70
12	14	36.8	45	10	US-09-893-615-71
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14	14	36.8	50	10	US-09-874-547-4
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19	14	36.8	50	10	US-09-874-547-11

20	14	36.8	50	10	US-09-874-547-12	Sequence 12, Appl
21	14	36.8	50	10	US-09-874-547-13	Sequence 13, Appl
22	14	36.8	51	10	US-09-874-547-8	Sequence 8, Appl
23	14	36.8	51	10	US-09-874-547-10	Sequence 10, Appl
24	14	36.8	52	10	US-09-874-547-46	Sequence 46, Appl
25	14	36.8	52	10	US-09-874-547-47	Sequence 47, Appl
26	14	36.8	52	10	US-09-874-547-57	Sequence 57, Appl
27	14	36.8	52	10	US-09-978-752-1	Sequence 1, Appl
28	14	36.8	53	9	US-09-968-5618-343	Sequence 343, App
29	14	36.8	53	10	US-09-968-5618-347	Sequence 347, App
30	14	36.8	53	10	US-09-874-547-37	Sequence 37, Appl
31	14	36.8	53	10	US-09-874-547-40	Sequence 40, Appl
32	14	36.8	53	10	US-09-874-547-41	Sequence 41, Appl
33	14	36.8	53	10	US-09-874-547-43	Sequence 43, Appl
34	14	36.8	53	10	US-09-874-547-50	Sequence 50, Appl
35	14	36.8	53	10	US-09-874-547-53	Sequence 53, Appl
36	14	36.8	53	10	US-09-874-547-56	Sequence 56, Appl
37	14	36.8	53	10	US-09-874-547-58	Sequence 58, Appl
38	14	36.8	53	10	US-09-874-547-59	Sequence 59, Appl
39	14	36.8	53	10	US-09-192-854-205	Sequence 205, App
40	14	36.8	53	10	US-09-192-854-209	Sequence 209, App
41	14	36.8	54	10	US-09-874-547-45	Sequence 45, Appl
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43	14	36.8	54	10	US-09-874-547-52	Sequence 52, Appl
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46	14	36.8	55	10	US-09-874-547-36	Sequence 36, Appl
47	14	36.8	55	10	US-09-874-547-38	Sequence 38, Appl
48	14	36.8	55	10	US-09-874-547-39	Sequence 39, Appl
49	14	36.8	55	10	US-09-874-547-42	Sequence 42, Appl
50	14	36.8	55	10	US-09-874-547-44	Sequence 44, Appl
51	14	36.8	55	10	US-09-874-547-48	Sequence 48, Appl
52	14	36.8	55	10	US-09-874-547-51	Sequence 51, Appl
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54	14	36.8	56	9	US-09-144-886-36	Sequence 36, Appl
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56	14	36.8	56	9	US-09-144-886-38	Sequence 38, Appl
57	14	36.8	56	9	US-09-144-886-39	Sequence 39, Appl
58	14	36.8	56	9	US-09-144-886-40	Sequence 40, Appl
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78	14	36.8	56	10	US-09-822-698A-39	Sequence 39, Appl
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84	14	36.8	307	10	US-09-878-574-14851	Sequence 14851, A
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86	14	36.8	673	9	US-09-854-133-479	Sequence 479, App
87	14	36.8	673	10	US-09-738-973-479	Sequence 479, App
88	14	36.8	750	10	US-09-730-374-1	Sequence 1, Appl
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90	14	36.8	930	12	US-10-052-798-6	Sequence 6, Appl
91	14	36.8	933	12	US-09-974-300-6951	Sequence 6951, Ap
92	14	36.8	933	12	US-10-052-798-8	Sequence 8, Appl

93 14 36.8 939 12 US-10-052-798-7 Sequence 7, Appli
c 94 14 36.8 1688 10 US-09-833-381-1988 Sequence 1988, Ap
95 14 36.8 4318 9 US-10-098-841-85 Sequence 85, Appl
96 14 36.8 18692 10 US-09-764-847-1682 Sequence 1682, Ap
97 13 34.2 33 10 US-09-753-436-36 Sequence 36, Appl
c 98 13 34.2 41 10 US-09-810-8368-13 Sequence 13, Appl
99 13 34.2 76 10 US-09-817-661-2 Sequence 2, Appli
c 100 13 34.2 108 10 US-09-923-876-4569 Sequence 4569, Ap

ALIGNMENTS

RESULT 1
US-09-929-060-4
; Sequence 4, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; PRIOR FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1329)
US-09-929-060-4

Query Match 42.1%; Score 16; DB 10; Length 1332;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 837 CGGCCATGGCGCAGGT 852

RESULT 2
US-09-929-060-5
; Sequence 5, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

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RESULT 3
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; Sequence 43, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-253-794-43

Query Match 36.8%; Score 14; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:48:53 ; Search time 30.3537 Seconds
(without alignments)
383.931 Million cell updates/sec

Title: US-09-424-705B-11

Perfect score: 38
Sequence: 1 cagccgcagcatgagcaggtscagctgcagagtcwag 38

Scoring table: OLIGO_NUC
Gapco 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16	42.1	1332	4	US-09-543-744-4	Sequence 4, Appl1
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4	16	42.1	1515	4	US-09-543-744-5	Sequence 5, Appl1
5	16	42.1	2363	1	US-07-923-724-7	Sequence 7, Appl1
6	16	42.1	2363	2	US-08-609-426A-7	Sequence 7, Appl1
7	16	42.1	2379	2	US-08-374-652C-1	Sequence 1, Appl1
8	15	39.5	703	4	US-08-998-416-671	Sequence 671, App
9	15	39.5	1173	2	US-08-614-156B-4	Sequence 4, Appl1
10	15	39.5	1173	4	US-09-213-864-1	Sequence 1, Appl1
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13	14	36.8	22	1	US-08-487-312-3	Sequence 3, Appl1
14	14	36.8	22	1	US-08-315-573-3	Sequence 3, Appl1
15	14	36.8	22	1	US-08-388-672A-4	Sequence 4, Appl1
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36	14	36.8	22	3	US-09-013-872-3	Sequence 3, Appl1
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52	14	36.8	31	2	US-08-764-938-6	Sequence 6, Appl1
53	14	36.8	31	3	US-09-131-052-6	Sequence 6, Appl1
54	14	36.8	31	4	US-09-131-053A-6	Sequence 6, Appl1
55	14	36.8	33	2	US-08-350-260A-549	Sequence 549, App
56	14	36.8	34	2	US-09-296-595-15	Sequence 15, Appl1
57	14	36.8	34	3	US-08-211-202-107	Sequence 107, App
58	14	36.8	38	2	US-08-273-146-24	Sequence 104, Appl1
59	14	36.8	41	4	US-09-813-781-60	Sequence 60, Appl1
60	14	36.8	45	2	US-08-814-806-20	Sequence 20, Appl1
61	14	36.8	45	4	US-09-813-781-3	Sequence 3, Appl1
62	14	36.8	45	4	US-08-448-418-10	Sequence 10, Appl1
63	14	36.8	46	2	US-08-458-218-37	Sequence 37, Appl1
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66	14	36.8	54	2	US-08-450-497-37	Sequence 37, Appl1
67	14	36.8	54	2	US-08-450-497-44	Sequence 44, Appl1
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71	14	36.8	54	1	US-08-458-218-44	Sequence 44, Appl1
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83	14	36.8	56	1	US-08-211-202-61	Sequence 61, Appl1
84	14	36.8	56	1	US-08-211-202-62	Sequence 62, Appl1
85	14	36.8	56	1	US-08-211-202-63	Sequence 63, Appl1
86	14	36.8	56	1	US-08-211-202-64	Sequence 64, Appl1
87	14	36.8	56	1	US-08-211-202-65	Sequence 65, Appl1
88	14	36.8	56	1	US-08-211-202-66	Sequence 66, Appl1
89	14	36.8	56	1	US-08-211-202-101	Sequence 101, App
90	14	36.8	56	1	US-08-211-202-102	Sequence 102, App
91	14	36.8	56	1	US-08-211-202-103	Sequence 103, App
92	14	36.8	56	1	US-08-211-202-104	Sequence 104, App
93	14	36.8	56	1	US-08-211-202-105	Sequence 105, App
94	14	36.8	56	1	US-08-211-202-106	Sequence 106, App
95	14	36.8	56	1	US-08-307-619-16	Sequence 16, Appl1
96	14	36.8	56	1	US-08-307-619-17	Sequence 17, Appl1
97	14	36.8	56	1	US-08-307-619-18	Sequence 18, Appl1
98	14	36.8	56	1	US-08-307-619-19	Sequence 19, Appl1
99	14	36.8	56	1	US-08-307-619-20	Sequence 20, Appl1
100	14	36.8	56	1	US-08-307-619-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

Query Match 42.1%; Score 16; DB 3; Length 1332;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCCATGGCGCAGGT 20
|||
Db 837 CGCCATGGCGCAGGT 852

RESULT 2
US-09-543-744-4
; Sequence 4, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-543-744-4

Query Match 42.1%; Score 16; DB 4; Length 1332;

Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCCATGGCGCAGGT 20
|||
Db 837 CGCCATGGCGCAGGT 852

RESULT 3
US-09-155-855-5
; Sequence 5, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-155-855-5

Query Match 42.1%; Score 16; DB 3; Length 1515;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGCCATGGCGCAGGT 20
|||
Db 1020 CGCCATGGCGCAGGT 1035

RESULT 4
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855